
WIREH (TW)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:35:27 1999; MasPar time 10.94 Seconds
Tabular output not generated. 464.471 Million cell updates/sec

Title: >US-09-079-785-6
Description: (1-239) from US09079785.pep
Perfect Score: 1719
Sequence: 1 MPEGLQAGSCGAPSPDAM.....DNTPLDNVLSFLYSSD 239

Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 32.791; Variance 153.921; scale 0.213

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1719	100.0	239	8 R45008	Sequence encoded by a	4.98e-142
2	1588	92.4	220	8 R45006	Sequence encoded by a	4.09e-130
3	1232	71.7	234	8 R45009	Sequence encoded by a	7.79e-98
4	1189	69.2	215	8 R45007	Sequence encoded by a	6.00e-94
5	113	6.6	137	14 R79087	Mouse Fas ligand (par	2.08e+00
6	113	6.6	138	14 R79088	Mouse Fas ligand (par	2.08e+00
7	113	6.6	179	14 R79085	Mouse Fas ligand (par	2.08e+00
8	113	6.6	279	18 R88357	Mouse Fas ligand.	2.08e+00
9	113	6.6	279	14 R79038	Mouse Fas ligand.	2.08e+00
10	113	6.6	279	14 R77282	Mouse Fas-L protein.	2.08e+00
11	107	6.2	397	2 P70261	Sequence of rat glia-	5.48e+00
12	101	5.9	137	14 R79085	Rat Fas ligand (parti	1.42e+01
13	101	5.9	138	14 R79083	Rat Fas ligand (parti	1.42e+01
14	101	5.9	179	14 R79066	Rat Fas ligand (parti	1.42e+01
15	101	5.9	278	14 R79095	Rat Fas ligand encode	1.42e+01
16	100	5.8	189	34 W29746	TNF related endotheli	1.66e+01

17	100	5.8	249	34 W29745	TNF related endotheli	1.66e+01
18	100	5.8	284	30 W47525	Homo sapiens tumour n	1.66e+01
19	99	5.8	690	37 W77414	Human sodium dependen	1.94e+01
20	98	5.7	149	2 R03264	Tumoricidal polypepti	2.27e+01
21	98	5.7	180	23 W10875	FasL/IT-alpha hybrid.	2.27e+01
22	94	5.5	130	14 R79096	Human Fas ligand C-te	4.20e+01
23	94	5.5	136	14 R88307	N-terminally deleted	4.20e+01
24	94	5.5	137	14 R88306	N-terminally deleted	4.20e+01
25	94	5.5	138	14 R79064	Human Fas ligand (par	4.20e+01
26	94	5.5	138	14 R88305	N-terminally deleted	4.20e+01
27	94	5.5	139	14 R88304	N-terminally deleted	4.20e+01
28	94	5.5	141	14 R88303	N-terminally deleted	4.20e+01
29	94	5.5	145	27 W35848	Human Fas-Ligand for	4.20e+01
30	94	5.5	151	26 W16667	Human Fas-Ligand (hfa	4.20e+01
31	94	5.5	178	14 R88308	C-terminally deleted	4.20e+01
32	94	5.5	265	33 W48954	Non-cleavable Fas lig	4.20e+01
33	94	5.5	268	33 W48953	Non-cleavable Fas lig	4.20e+01
34	94	5.5	281	14 R77281	Human Fas-L protein.	4.20e+01
35	94	5.5	281	26 W27143	Human Fas-Ligand.	4.20e+01
36	94	5.5	281	35 W49105	Fas Ligand.	4.20e+01
37	94	5.5	281	36 W75959	Human Fas ligand.	4.20e+01
38	94	5.5	281	18 R98104	Human Fas ligand deri	4.20e+01
39	94	5.5	281	18 R88356	Human Fas ligand.	4.20e+01
40	94	5.5	287	26 W27146	CH3/Fas ligand domain	4.20e+01
41	95	5.5	374	32 W63694	Human secreted protei	3.61e+01
42	94	5.5	378	27 W35864	Human Fas-Ligand:IGG2	4.20e+01
43	94	5.5	397	4 R20089	PN-I alpha analogue.	4.20e+01
44	94	5.5	397	4 R20090	Sequence of protease	4.20e+01
45	94	5.5	397	4 R20086	PN-I alpha analogue.	4.20e+01

ALIGNMENTS

RESULT 1
ID R45008 standard; Protein: 239 AA.
AC R45008;
DT 19-JUN-1994 (first entry)
DE Sequence encoded by a murine CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
OS Acromys cahirinus.
FH Key Location/Qualifiers
FT region 47..67.
FT /label= Transmembrane
FN W0324135-A.
PD 09-DEC-1993.
PF 25-MAY-1993; U04926.
PR 26-MAY-1992; US-889717.
PR 02-JUN-1992; US-892459.
PR 15-JUN-1992; US-899660.
PR 01-JUL-1992; US-907224.
PR 27-OCT-1992; US-966775.
PA (IMV) IMMUNEX CORP.
PI Armitage RJ, Goodwin RG, Smith CA;
DR WPI; 93-405417/50.
DR N-ESDB; Q53537.
PT New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy.
PS Claim 15; Figure 6a; 59pp; English.
CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prepd. from
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC (Q53535). This cDNA can then be used as a probe to screen a human PBL
CC cDNA library to obtain cDNA encoding human CD30-L (Q53536). An anchored
CC PCR technique was employed to isolate CD30-L human and murine clones
CC containing an additional 19 N-terminal amino acid sequence (Q53537,

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CC Q53538).
SQ Sequence 239 AA;

Query Match 100.0%; Score 1719; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.98e-142;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mepglqagscgapsdpamqvpgsvasprstprstsrsvfystaltalvclvvava 60
QY 1 MEPGLQAGSCGAPSDPAMQVPGSVASPRSTRPRSTRSRVYFYSTALTALVCLVVAVA 60

Db 61 ilvlvqvkkdstpntekaplkgnccsedlftclktstpskkswaylqvskhlnntklsw 120
QY 61 IILVLVQVKKDSPTNTEKAPLKGNCCSEDLFTCLKTSTPSKKSWAYLQVSKHLNNTKLSW 120

Db 121 nedgtlhglydgnllyqfpglyfvcqlqfvcqsnhsdvdtlqlinskkkqtlvt 180
QY 121 NEDGTLHGLYDGNLIVQFPGLYFVCQLQFVCQSNHSVDLTLQLINSKKKQTLVT 180

Db 181 vcesgvqskniyqnlsgfllyhlyqvnstisrvdnfgyvdtntfpldnvlsvflysssd 239
QY 181 VCESGVQSKNIYQNLQSGFLHLYQVNSTISVRVDFGYVDTNFPDNLVLSVFLYSSSD 239

RESULT 2
ID R45006 standard; Protein; 220 AA.
AC R45006;
DT 19-JUN-1994 (first entry)
DE Sequence encoded by a murine CD30-L cDNA clone.
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
OS Acromyca cahirinus.
FH Key Location/Qualifiers
FT region 28..48 /label= transmembrane
PI WO9324135-A.
PD 09-DEC-1993.
PF 25-MAY-1993; U04926.
PR 26-MAY-1992; US-889717.
PR 02-JUN-1992; US-892459.
PR 15-JUN-1992; US-899660.
PR 01-JUL-1992; US-907224.
PR 27-OCT-1992; US-966775.
PA (IMV ) IMMUNEX CORP.
PI Armitage RJ, Goodwin RG, Smith CA;
DR WPI; 93-405417/50.
DR N-PSDB; Q53535.
PT New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
PS Claim 15; Figure 3a; 59pp; English.
CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prep'd from
CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC (Q53535). This cDNA can then be used as a probe to screen a human PBL
CC cDNA library to obtain cDNA encoding human CD30-L.
CC This cDNA can then be used as a probe to screen a human PBL cDNA
CC library to obtain cDNA encoding human CD30-L.
SQ Sequence 220 AA;

Query Match 92.4%; Score 1588; DB 8; Length 220;
Best Local Similarity 100.0%; Pred. No. 4.09e-130;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mvqpgsvasprstprstsrsvfystaltalvclvvavaillvqvkkdstpnttek 60
QY 20 MVQPGSVASPRSTRPRSTRSRVYFYSTALTALVCLVVAVAILLVQVKKDSPTNTEK 79

Db 61 aplkgnccsedlftclktstpskkswaylqvskhlnntklswnedgtlhglydgnllyq 120
QY 61 APLKGNCCSEDLFTCLKTSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHLGYDGNLIVQ
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QY 80 APLKGNCCSEDLFTCLKTSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHLGYDGNLIVQ 139
Db 121 fpglyfvcqlqfvcqsnhsdvdtlqlinskkkqtlvtvcesgvqskniyqnlsgfl 180
QY 140 FPGLYFVCQLQFVCQSNHSVDLTLQLINSKKKQTLVTVCESGVQSKNIYQNLQSGFL 199
Db 181 lhyiqvnstisrvdnfgyvdtntfpldnvlsvflysssd 220
QY 200 LHYIQVNSTISVRVDFGYVDTNFPDNLVLSVFLYSSSD 239

RESULT 3
ID R45009 standard; Protein; 234 AA.
AC R45009;
DT 19-JUN-1994 (first entry)
DE Sequence encoded by a human CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
OS Homo sapiens.
FH Key Location/Qualifiers
FT region 41..62 /label= Transmembrane
PI WO9324135-A.
PD 09-DEC-1993.
PF 25-MAY-1993; U04926.
PR 26-MAY-1992; US-889717.
PR 02-JUN-1992; US-892459.
PR 15-JUN-1992; US-899660.
PR 01-JUL-1992; US-907224.
PR 27-OCT-1992; US-966775.
PA (IMV ) IMMUNEX CORP.
PI Armitage RJ, Goodwin RG, Smith CA;
DR WPI; 93-405417/50.
DR N-PSDB; Q53538.
PT New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
PS Claim 15; Figure 7a; 59pp; English.
CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prep'd from
CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC (Q53535). This cDNA can then be used as a probe to screen a human PBL
CC cDNA library to obtain cDNA encoding human CD30-L (Q53536). An anchored
CC PCR technique was employed to isolate CD30-L human and murine clones
CC containing an additional 19 N-terminal amino acid sequence (Q53537,
CC Q53538).
SQ Sequence 234 AA;

Query Match 71.7%; Score 1232; DB 8; Length 234;
Best Local Similarity 70.0%; Pred. No. 7.79e-98;
Matches 168; Conservative 39; Mismatches 26; Indels 7; Gaps 3;

Db 1 mdpqlqalngmappgdtamhvpagsvashl-gt-----tsrsfylltatlalclvftv 54
QY 1 MEPQLQAGSCGAPSDPAMQVPGSVASPRSTRPRSTRSRVYFYSTALTALVCLVVAV 59

Db 55 atimlvvqvrttdslpnspdnvplkgnccsedlcllrapfkkswaylqvskhlnntklsl 114
QY 60 AITILVLVQVKKDSPTNTEKAPLKGNCCSEDLFTCLKTSTPSKKSWAYLQVSKHLNNTKLS 119

Db 115 wnkdgllhgvrydgnllyqfpglyfvcqlqfvcqsnhsdvdtlqlinskkkqtlvt 174
QY 120 WNEDGTLHGLYDGNLIVQFPGLYFVCQLQFVCQSNHSVDLTLQLINSKKKQTLV 179

Db 175 tvcesgmqtthvynqnlsgfllydqvnttisrvdnfgyvdtntfpldnvlsvflysssd 234
QY 180 TVCESGVQSKNIYQNLQSGFLHLYQVNSTISVRVDFGYVDTNFPDNLVLSVFLYSSSD 239
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PR 10-NOV-1993; JP-305975.
PR PR 13-DEC-1993; JP-342526.
PR PR 18-MAR-1994; JP-074344.
PR PR 08-JUL-1994; JP-180955.
PR PR 07-SEP-1994; JP-239363.
PR PR 18-OCT-1994; JP-278378.
PA (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
PI Nagata S, Nakamura N, Suda T, Takahashi T;
DR N-PSDB; Q99496.
PT Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto-immune diseases
PS Claim 9; Page 219-221; 300pp; Japanese.
CC Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the mouse Fas ligand.
SQ Sequence 137 AA;

Query Match 6.6%; Score 113; DB 14; Length 137;
Best Local Similarity 32.3%; Pred. No. 2.08e+00;
Matches 20; Conservative 14; Mismatches 24; Indels 4; Gaps

Db 3 ahltgnphrsiplewedygtaligvkykkgvlvinetglyfvsykvfyrgscnnqp 62
QY ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
105 AYLQVSKHLNNTKLSWNE-DGT--IHGLIYODGNLIVQFPGLYFIVCOLQLVQ-CSNHS 16
Db 63 ln 64
QY ::
161 VD 162

RESULT 6
ID R79088 standard; Protein; 138 AA.
AC R79088;
DT 22-FEB-1996 (first entry)
DE Mouse Fas ligand (partial sequence).
KE Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; Fas-L; mouse.
OS Mus musculus.
PN W09513293-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; J01899.
PR 10-NOV-1993; JP-305975.
PR 13-DEC-1993; JP-342526.
PR 18-MAR-1994; JP-074344.
PR 08-JUL-1994; JP-180955.
PR 07-SEP-1994; JP-239363.
PR 18-OCT-1994; JP-278378.
PA (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
PI Nagata S, Nakamura N, Suda T, Takahashi T;
DR N-PSDB; Q99497.
PT Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto-immune diseases
PS Claim 10; Page 221-222; 300pp; Japanese.
CC Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the mouse Fas ligand.
SQ Sequence 138 AA;

Query Match 6.6%; Score 113; DB 14; Length 138;
Best Local Similarity 32.3%; Pred. No. 2.08e+00;
Matches 20; Conservative 14; Mismatches 24; Indels 4; Gaps

Db 4 ahltgnphrsiplewedygtaligvkykkgvlvinetglyfvsykvfyrgscnnqp 63
QY ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
105 AYLQVSKHLNNTKLSWNE-DGT--IHGLIYODGNLIVQFPGLYFIVCOLQLVQ-CSNHS 16
Db 64 ln 65

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10


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Db 145 ahltnphrsrslpewdtygtalisgvykkgglvlnetgfyfvykvyfrgscnnp 204
QY 105 AYLVQSKHLNKLNSWED-GT--IHGLIYQDGNLIVQFPGLYFIVCOLQFLVQ-CSNHS 160

Db 205 ln 206
QY 161 VD 162

RESULT 10
ID R77282 standard; Protein; 279 AA.
AC R77282; 1995 (first entry)
DE Mouse Fas-L protein.
KW Fas ligand; Fas-L; cell surface protein; autoimmune disease;
KW self-tolerance.
OS Mus sp.
FH Key Location/Qualifiers
FT Domain 1..78
FT FT /label= Cytoplasmic_domain
FT domain 79..103
FT FT /label= Transmembrane_domain
FT domain 104..279
FT FT /label= Extracellular_domain
PN WO9518819-A.
PD 13-JUL-1995.
PF 06-JAN-1995; U00362.
PR 07-JAN-1994; US-179138.
PR 01-FEB-1994; US-190559.
PA (IMV ) IMMUNEX CORP.
PI Goodwin RG;
DR WPI; 95-255032/33.
DR N-PSDB; Q91312.
PT Human and murine DNA encoding ligand(s) binding to cell surface protein
PT Fas - useful for studying auto-immune disorder(s) and development of
PT self-tolerance.
PS Disclosure; Page 29-30; 38pp; English.
CC A cDNA library prep. from mouse peripheral blood lymphocyte mRNA was
CC screened with a murine Fas-L probe from the 3' end of Fas-L DNA.
CC An isolated clone (Q91312) encoded mouse Fas-L.
SQ Sequence 279 AA;

Query Match 6.6%; Score 113; DB 14; Length 279;
Best Local Similarity 32.3%; Pred. No. 2.08e+00;
Matches 20; Conservative 14; Mismatches 24; Indels 4; Gaps 3;

Db 145 ahltnphrsrslpewdtygtalisgvykkgglvlnetgfyfvykvyfrgscnnp 204
QY 105 AYLVQSKHLNKLNSWED-GT--IHGLIYQDGNLIVQFPGLYFIVCOLQFLVQ-CSNHS 160

Db 205 ln 206
QY 161 VD 162

RESULT 11
ID P70261 standard; Protein; 397 AA.
AC P70261;
DE 29-MAY-1991 (first entry)
DE Sequence of rat glia-derived neurite-promoting factor (GdNPF).
KW Nerve fibre regeneration; neurite promoter;
KW serine protease inhibitor.
OS Rat.
FH Key Location/Qualifiers
FT Peptide 1..19
FT FT /notes="may be omitted"
FT protein 20..397
PN EP-233838-A.
PD 26-AUG-1987.
PF 29-JAN-1987; 810057.
PR 04-FEB-1986; GB-002626.
PR 11-FEB-1986; GB-003354.
PR 31-JUL-1986; GB-018760.

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PA (CIBA ) CIBA GEIGY AG.
PI Monard D, Odink KG, Gloor S;
DR WPI; 87-236863/34.
DR N-PSDB; N70395.
PT Recombinant human glia derived neurite-promoting factor - used
PT for promoting nerve fibre regeneration following lesions in the
PT nervous system
PS Disclosure; pp26-28; 36pp; English.
CC For the prepn. of human GdNPF, the cDNA library is pref. derived
CC from human glioma cells, eg from the human glioma cell line LN340.
CC For the prepn. of related peptides, eg rat GdNPF, other glial cells,
CC eg c6 rat glioma cells, are used to prepare a cDNA library. The
CC neurite-promoting and serine protease-inhibiting properties of
CC GdNPF, related peptides and fragments make them useful for promoting
CC nerve fibre regeneration following lesions in the nervous system.
CC and for interfering with the migration of normal and tumour cells.
SQ Sequence 397 AA;

Query Match 6.2%; Score 107; DB 2; Length 397;
Best Local Similarity 30.1%; Pred. No. 5.48e+00;
Matches 31; Conservative 26; Mismatches 41; Indels 5; Gaps 5;

Db 285 vpkrmqlvlpkftalqtdlkepkalgite-ifepskanfakitrseelshvhlqkak 343
QY 59 VAIILVLVQKKDSTPNTTERKAPLKGNCSEDLFCTLKSTPSKSWA-YLVQSKHLNNTK 117

Db 344 levsedgtkaavv-ttailarsppwfv-drpflf-cirhn 383
QY 118 LSWNEDGTIHGLIYQDGNLIVQFPGLYFIVCOLQFLVQCSNHS 160

RESULT 12
ID R79065 standard; Protein; 137 AA.
AC R79065;
DE 22-FEB-1996 (first entry)
DE Rat Fas ligand (partial sequence).
KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; Fas-L; rat.
OS Rattus rattus.
PN WO9513293-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; J01899.
PR 10-NOV-1993; JP-305975.
PR 13-DEC-1993; JP-342526.
PR 18-MAR-1994; JP-074344.
PR 08-JUL-1994; JP-180955.
PR 07-SEP-1994; JP-239363.
PR 18-OCT-1994; JP-278378.
PA (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
PI Nagata S, Nakamura N, Suda T, Takahashi T;
DR WPI; 95-194031/25.
DR N-PSDB; Q99494.
PT Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto-immune diseases
PS Claim 5; Page 212-213; 300pp; Japanese.
CC Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the rat Fas ligand.
SQ Sequence 137 AA;

Query Match 5.9%; Score 101; DB 14; Length 137;
Best Local Similarity 33.3%; Pred. No. 1.42e+01;
Matches 16; Conservative 13; Mismatches 15; Indels 4; Gaps 3;

Db 16 lewdtygtalisgvykkgglvlnetgfyfvykvyfrgscnnp 63
QY 118 LSWNED-GT--IHGLIYQDGNLIVQFPGLYFIVCOLQFLVQ-CSNHS 161

RESULT 13
ID R79065 standard; Protein; 138 AA.

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[illegible]

W P S R L A

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:38:44 1999; MagPar time 4.00 Seconds
Tabular output not generated.
607.121 Million cell updates/sec

Title: >US-09-079-785-6
Description: (1-239) from US09079785.pep
Perfect Score: 1719
Sequence: 1 MEPLQAGSCGAPDPAM.....DNTFPLDNLVLYSSSD 239

Scoring table: PAM 150
Gap 11

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 30.540; Variance 144.384; scale 0.212

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1719	100.0	239	2	US-08-580- Sequence 6, Applicatio	4.73e-142
2	1719	100.0	239	1	US-08-570- Sequence 6, Applicatio	4.73e-142
3	1719	100.0	239	1	US-08-225- Sequence 6, Applicatio	4.73e-142
4	1588	92.4	220	2	US-08-580- Sequence 19, Applicati	3.32e-130
5	1588	92.4	220	1	US-08-225- Sequence 19, Applicati	3.32e-130
6	1588	92.4	220	1	US-08-570- Sequence 19, Applicati	3.32e-130
7	1232	71.7	234	1	US-08-225- Sequence 8, Applicatio	4.21e-98
8	1232	71.7	234	1	US-08-570- Sequence 8, Applicatio	4.21e-98
9	1232	71.7	234	2	US-08-580- Sequence 8, Applicatio	4.21e-98
10	1189	69.2	215	1	US-08-570- Sequence 23, Applicati	3.09e-94
11	1189	69.2	215	2	US-08-580- Sequence 23, Applicati	3.09e-94
12	1189	69.2	215	1	US-08-225- Sequence 21, Applicati	6.70e-73
13	951	55.3	130	2	US-08-580- Sequence 21, Applicati	6.70e-73
14	951	55.3	130	1	US-08-225- Sequence 21, Applicati	6.70e-73
15	951	55.3	130	1	US-08-570- Sequence 21, Applicati	6.70e-73
16	564	32.8	125	2	US-08-580- Sequence 20, Applicati	1.40e-38
17	564	32.8	125	1	US-08-570- Sequence 20, Applicati	1.40e-38
18	564	32.8	125	1	US-08-225- Sequence 20, Applicati	1.40e-38
19	113	6.6	279	3	PCT-US95-0 Sequence 5, Applicatio	7.08e-01
20	94	5.5	281	3	US-08-810- Sequence 2, Applicatio	1.52e+01
21	94	5.5	281	3	PCT-US95-0 Sequence 2, Applicatio	1.52e+01
22	94	5.5	397	4	Patent No. 5187089	1.52e+01
23	94	5.5	397	4	Patent No. 5187089-2	1.52e+01

24	91	5.3	158	1	US-08-397- Sequence 9, Applicatio	2.43e+01
25	91	5.3	158	1	US-07-794- Sequence 9, Applicatio	2.43e+01
26	91	5.3	158	1	US-07-794- Sequence 12, Applicati	2.43e+01
27	91	5.3	158	1	US-08-397- Sequence 12, Applicati	2.43e+01
28	91	5.3	397	4	5495001-7 Patent No. 5495001	2.43e+01
29	91	5.3	397	4	5457090-2 Patent No. 5457090	2.43e+01
30	90	5.2	128	2	US-08-426- Sequence 14, Applicati	2.84e+01
31	90	5.2	158	1	US-08-397- Sequence 7, Applicatio	2.84e+01
32	90	5.2	158	1	US-07-794- Sequence 7, Applicatio	2.84e+01
33	89	5.2	158	1	US-07-994- Sequence 99, Applicati	3.31e+01
34	89	5.2	353	1	US-08-073- Sequence 17, Applicati	3.31e+01
35	89	5.2	380	1	US-08-073- Sequence 18, Applicati	3.31e+01
36	90	5.2	397	4	5187089-10 Patent No. 5187089	2.84e+01
37	89	5.2	416	1	US-08-073- Sequence 2, Applicatio	3.31e+01
38	90	5.2	585	4	5475086-6 Patent No. 5475086	2.84e+01
39	90	5.2	777	2	US-08-477- Sequence 4, Applicatio	2.84e+01
40	90	5.2	779	2	US-08-426- Sequence 24, Applicati	2.84e+01
41	90	5.2	779	2	US-08-426- Sequence 4, Applicatio	2.84e+01
42	90	5.2	836	2	US-08-426- Sequence 6, Applicatio	2.84e+01
43	90	5.2	837	2	US-08-426- Sequence 23, Applicati	2.84e+01
44	88	5.1	584	1	US-08-161- Sequence 2, Applicatio	3.86e+01
45	88	5.1	585	2	US-08-484- Sequence 58, Applicati	3.86e+01

ALIGNMENTS

RESULT 1
ID US-08-580-014-6 STANDARD; PRT; 239 AA.
XX
AC
XX
DT
XX
DE
XX
Sequence 6, Application US/08580014
Sequence 6, Application US/08580014
Patent No. 5753203
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Armitage, Richard J.
APPLICANT: Gruss, Hans-Jurgen
TITLE OF INVENTION: No. 5753203e1 Cytokine That Binds CD30
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Seese, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,014
FILING DATE: 20-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:

CC	APPLICATION NUMBER:	US/08/570,923
CC	FILING DATE:	12-DEC-1995
CC	CLASSIFICATION:	530
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/08/225,989
CC	FILING DATE:	12 APRIL 1994
CC	APPLICATION NUMBER:	US 07/966,775
CC	FILING DATE:	27-OCT-1992
CC	CLASSIFICATION:	530
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 907,224
CC	FILING DATE:	01-JUL-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 899,660
CC	FILING DATE:	15-JUN-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 892,459
CC	FILING DATE:	02-JUN-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 889,717
CC	FILING DATE:	26-MAY-1992
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Seese, Kathryn A.
CC	REGISTRATION NUMBER:	32,172
CC	REFERENCE/DOCKET NUMBER:	2804-E
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	(206)587-0430
CC	TELEFAX:	(206)233-0644
CC	TELEX:	756822
CC	INFORMATION FOR SEQ ID NO:	6:
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	239 amino acids
CC	TYPE:	amino acid
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	protein
SQ	SEQUENCE	239 AA; 26519 MW; 334382 CN;
Query Match 100.0%; Score 1719; DB 1; Length 239;		
Best Local Similarity 100.0%; Pred. No. 4.73e-142;		
Matches 239; Conservative: 0; Mismatches 0; Indels 0; Gaps 0;		
D b	1	MEPGLQAGSCGAPSPDPAMQVPGSVASFPWRSTRPWRSTSRSYFYLTALVCLVVAVA 60
Q y	1	MEPGLQAGSCGAPSPDPAMQVPGSVASFPWRSTRPWRSTSRSYFYLTALVCLVVAVA 60
D b	61	IILVLVYVKKDDSTPNTEKAPLAKGGNCSEDLFTCLKSTPSKKSWAYLOYSKHNLNNTKLSW 120
Q y	61	IILVLVYVKKDDSTPNTEKAPLAKGGNCSEDLFTCLKSTPSKKSWAYLOYSKHNLNNTKLSW 120
D b	121	NEDGTIHLGYDGNLIIVPPGLYFIVCQLFLVCQSNSHSVDLTLLQLINSIKKQTLYT 180
Q y	121	NEDGTIHLGYDGNLIIVPPGLYFIVCQLFLVCQSNSHSVDLTLLQLINSIKKQTLYT 180
D b	181	VCEGSVGSKNIYNQLSOFLLHYLQVNSTISVRVDNFQQYYVDTNTPFDLNVLVSFLYSSSD 239
Q y	181	VCEGSVGSKNIYNQLSOFLLHYLQVNSTISVRVDNFQQYYVDTNTPFDLNVLVSFLYSSSD 239
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ID	US-08-225-989-6	STANDARD; PRT; 239 AA.
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AC		
XX		
DT		
XX		
DE	Sequence 6, Application US/08225989	
CC	Sequence 6, Application US/08225989	
CC	Patent No. 5480981	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Goodwin, Raymond G.	
CC	APPLICANT: Smith, Craig A.	
CC	APPLICANT: Armitage, Richard J.	

CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 239 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 239 AA; 26519 MW; 334382 CN;
Query Match 100.0%; Score 1719; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.73e-142;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MEPGLQAGSCGAPSDPAMQVPGSVASVPSRSTRPWRSTRSRFYLSLTALVCLVVA 60
QY 1 MEPGLQAGSCGAPSDPAMQVPGSVASVPSRSTRPWRSTRSRFYLSLTALVCLVVA 60

Db 61 IILVLYVQKDSPTNTEKAPLKGNCSEDLFCTLSTPSKSWAYLQVSKHLNNTKLSW 120
QY 61 IILVLYVQKDSPTNTEKAPLKGNCSEDLFCTLSTPSKSWAYLQVSKHLNNTKLSW 120

Db 121 NEDGTGHLIYQDGLVQPGGLFYFVQQLVQCSNHSVDLTQLLINSKIKKQTLVT 180
QY 121 NEDGTGHLIYQDGLVQPGGLFYFVQQLVQCSNHSVDLTQLLINSKIKKQTLVT 180

Db 181 VCESGVQSNKNIYNLSQFLHLYLQVNSTISVRVDNFQYVDNTFPDLNLSVLYSSSD 239
QY 181 VCESGVQSNKNIYNLSQFLHLYLQVNSTISVRVDNFQYVDNTFPDLNLSVLYSSSD 239

RESULT 4

ID XX US-08-580-014-19 STANDARD: PRT; 220 AA.
AC XXXXXX
XX
DT
XX
DE Sequence 19, Application US/08580014
XX Sequence 19, Application US/08580014
CC Patent No. 5753203
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580,014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 19:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 220 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 220 AA; 24724 MW; 283693 CN;
Query Match 92.4%; Score 1588; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. NO. 3.32e-130;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MQVQPGSVASVPSRSTRPWRSTRSRFYLSLTALVCLVVAIILVLYVQKDSPTNTEK 60
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QY	20	MQVQGVASBWRSTRPWRSTSRSYFYFLSTALTALVCLVAVAILVLVQKDKDTPNTTEK	79
Db	61	APLKGKGCSEDLFCTLKASTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ	120
QY	80	APLKGKGCSEDLFCTLKASTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ	139
Db	121	FPGLYFIVCOLQFLVQCSNHSVDLTTQLLINSIKKQOTLVTVCESGVQSKNIYQNL	180
QY	140	FPGLYFIVCOLQFLVQCSNHSVDLTTQLLINSIKKQOTLVTVCESGVQSKNIYQNL	199
Db	181	LHYLQVNSTISVRVDFNQYVDNTFPLDNVLSVFLYSSD	220
QY	200	LHYLQVNSTISVRVDFNQYVDNTFPLDNVLSVFLYSSD	239
RESULT	5		
ID	US-08-225-989-19	STANDARD;	PRT; 220 AA.
XX	xxxxxx		
AC			
XX			
DT			
XX			
XX			
DE	Sequence 19, Application US/08225989		
XX			
CC	Sequence 19, Application US/08225989		
CC	Patent No. 5480981		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Goodwin, Raymond G.		
CC	APPLICANT: Smith, Craig A.		
CC	APPLICANT: Armitage, Richard J.		
CC	APPLICANT: Gruss, Hans-Jurgen		
CC	TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30		
CC	NUMBER OF SEQUENCES: 23		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Kathryn A. Seese, Immunex Corporation		
CC	STREET: 51 University Street		
CC	CITY: Seattle		
CC	STATE: Washington		
CC	COUNTRY: USA		
CC	ZIP: 98101		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: Apple Macintosh		
CC	OPERATING SYSTEM: Apple 7.1		
CC	SOFTWARE: Microsoft Word, Version 5.1a		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/225,989		
CC	FILING DATE: 12 APRIL 1994		
CC	CLASSIFICATION: 435		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 07/966,775		
CC	FILING DATE: 27-OCT-1992		
CC	CLASSIFICATION: 435		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 907,224		
CC	FILING DATE: 01-JUL-1992		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 899,660		
CC	FILING DATE: 15-JUN-1992		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 892,459		
CC	FILING DATE: 02-JUN-1992		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US 889,717		
CC	FILING DATE: 26-MAY-1992		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Seese, Kathryn A.		
CC	REGISTRATION NUMBER: 32,172		
CC	REFERENCE/DOCKET NUMBER: 2804-E		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: (206)587-0430		
CC	TELEFAX: (206)233-0644		
CC	TELEX: 756822		

CC	APPLICATION NUMBER:	US 899,660
CC	FILING DATE:	15-JUN-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 892,459
CC	FILING DATE:	02-JUN-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 889,717
CC	FILING DATE:	26-MAY-1992
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Seese, Kathryn A.
CC	REGISTRATION NUMBER:	32,172
CC	REFERENCE/DOCKET NUMBER:	2804-E
CC	TELEPHONE:	(206)587-0430
CC	TELEFAX:	(206)233-0644
CC	INFORMATION FOR SEQ ID NO:	19:
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	220 amino acids
CC	TYPE:	amino acid
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	protein
CC	SEQUENCE	220 AA; 24724 MW; 283593 CN;
SQ	Query Match	92.4%; Score 1588; DB 1; Length 220;
	Best Local Similarity	100.0%; Pred. No. 3.32e-130;
	Mismatches	220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dd	1	MOVQGSVSPWRSRPRSRPSTALVCLVAVALVLVVKDKSTPTTEK 60
Qy	20	MOVQGSVSPWRSRPRSRPSTALVCLVAVALVLVVKDKSTPTTEK 79
Dd	61	APLKGNCSEDLFCFLKTPSKSWAYLOVSKHLNKLWNEDGTIHLGIYODGNLIQV 120
Qy	80	APLKGNCSEDLFCFLKTPSKSWAYLOVSKHLNKLWNEDGTIHLGIYODGNLIQV 139
Dd	121	FPGLYFIVCOLQLVQCNSHSDVLTLLQLINSIKKQTTLVTVCESGVQSKNIYQNLSQFL 180
Qy	140	FPGLYFIVCOLQLVQCNSHSDVLTLLQLINSIKKQTTLVTVCESGVQSKNIYQNLSQFL 199
Dd	181	LHYLVNSTISVRVDNFQYDNTFFPLDNVLSVFLYSSTD 220
Qy	200	LHYLVNSTISVRVDNFQYDNTFFPLDNVLSVFLYSSTD 239
RESULT	7	
ID	US-08-225-989-8	STANDARD; PRT: 234 AA.
XX	xxxxxx	
DT	Sequence 8, Application US/08225989	
DE	Sequence 8, Application US/08225989	
CC	Patent No. 5480981	
CC	GENERAL INFORMATION:	
CC	APPLICANT:	Goodwin, Raymond G.
CC	APPLICANT:	Smith, Craig A.
CC	APPLICANT:	Armitage, Richard J.
CC	APPLICANT:	Gruess, Hans-Jurgen
CC	TITLE OF INVENTION:	No. 5480981el Cytokine That Binds CD30
CC	NUMBER OF SEQUENCES:	23
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE:	Kathryn A. Seese, Immunex Corporation
CC	STREET:	51 University Street
CC	City:	Seattle
CC	STATE:	Washington
CC	COUNTRY:	USA
CC	ZIP:	98101
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	Apple Macintosh

CC	APPLICATION NUMBER: US 899,660	CC	OPERATING SYSTEM: Apple 7.1
CC	FILING DATE: 15-JUN-1992	CC	SOFTWARE: Microsoft Word, Version 5.1a
CC	PRIOR APPLICATION DATA:	CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US 892,459	CC	APPLICATION NUMBER: US/08/225,989
CC	FILING DATE: 02-JUN-1992	CC	FILING DATE: 12 APRIL 1994
CC	PRIOR APPLICATION DATA:	CC	CLASSIFICATION: 435
CC	APPLICATION NUMBER: US 889,717	CC	PRIOR APPLICATION DATA:
CC	FILING DATE: 26-MAY-1992	CC	APPLICATION NUMBER: US 07/966,775
CC	ATTORNEY/AGENT INFORMATION:	CC	FILING DATE: 27-OCT-1992
CC	NAME: Seese, Kathryn A.	CC	CLASSIFICATION: 435
CC	REGISTRATION NUMBER: 32,172	CC	PRIOR APPLICATION DATA:
CC	REFERENCE/DOCKET NUMBER: 2804-E	CC	APPLICATION NUMBER: US 899,660
CC	TELEPHONE: (206)587-0430	CC	FILING DATE: 15-JUN-1992
CC	TELEFAX: (206)233-0644	CC	PRIOR APPLICATION DATA:
CC	INFORMATION FOR SEQ ID NO: 19:	CC	APPLICATION NUMBER: US 892,459
CC	SEQUENCE CHARACTERISTICS:	CC	FILING DATE: 02-JUN-1992
CC	LENGTH: 220 amino acids	CC	PRIOR APPLICATION DATA:
CC	TYPE: amino acid	CC	APPLICATION NUMBER: US 889,717
CC	TOPOLOGY: linear	CC	FILING DATE: 26-MAY-1992
CC	MOLECULE TYPE: protein	CC	ATTORNEY/AGENT INFORMATION:
CC	SEQUENCE 220 AA; 24724 MW; 283593 CN;	CC	NAME: Seese, Kathryn A.
CC	Query Match 92.4%; Score 1588; DB 1; Length 220;	CC	REGISTRATION NUMBER: 32,172
CC	Best Local Similarity 100.0%; Pred. No. 3.32e-130;	CC	REFERENCE/DOCKET NUMBER: 2804-E
CC	Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	TELEPHONE: (206)587-0430
CC	1 MQVQGSVSPWRSRPSRSTALVCLVAVAILVLVQKSDPTNTEK 60	CC	TELEFAX: (206)233-0644
CC	20 MQVQGSVSPWRSRPSRSTALVCLVAVAILVLVQKSDPTNTEK 79	CC	INFORMATION FOR SEQ ID NO: 19:
CC	61 APLKGCSEDLFCFLKTPSKKSWAYLQVSKHLNKLWNEDGTIHLIYQDGLIYQ 120	CC	SEQUENCE CHARACTERISTICS:
CC	80 APLKGCSEDLFCFLKTPSKKSWAYLQVSKHLNKLWNEDGTIHLIYQDGLIYQ 139	CC	LENGTH: 220 amino acids
CC	121 FPGLYFIVCOLQFLVQCSNHSVDLFLQLLINSKIKQTLLVTVCSGVQSKNIYQNSQFL 180	CC	TYPE: amino acid
CC	140 FPGLYFIVCOLQFLVQCSNHSVDLFLQLLINSKIKQTLLVTVCSGVQSKNIYQNSQFL 199	CC	TOPOLOGY: linear
CC	181 LHYLVNSTISVRVDNFOYDNTNFPDLNVLVSFLYSSD 220	CC	MOLECULE TYPE: protein
CC	200 LHYLVNSTISVRVDNFOYDNTNFPDLNVLVSFLYSSD 239	CC	SEQUENCE 220 AA; 24724 MW; 283593 CN;
CC	RESULT 7	CC	Query Match 92.4%; Score 1588; DB 1; Length 220;
CC	ID US-08-225-989-8 STANDARD; PRT: 234 AA.	CC	Best Local Similarity 100.0%; Pred. No. 3.32e-130;
CC	xxxxxx	CC	Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	Sequence 8, Application US/08225989	CC	1 MQVQGSVSPWRSRPSRSTALVCLVAVAILVLVQKSDPTNTEK 60
CC	Patent No. 5480981	CC	20 MQVQGSVSPWRSRPSRSTALVCLVAVAILVLVQKSDPTNTEK 79
CC	GENERAL INFORMATION:	CC	61 APLKGCSEDLFCFLKTPSKKSWAYLQVSKHLNKLWNEDGTIHLIYQDGLIYQ 120
CC	APPLICANT: Goodwin, Raymond G.	CC	80 APLKGCSEDLFCFLKTPSKKSWAYLQVSKHLNKLWNEDGTIHLIYQDGLIYQ 139
CC	APPLICANT: Smith, Craig A.	CC	121 FPGLYFIVCOLQFLVQCSNHSVDLFLQLLINSKIKQTLLVTVCSGVQSKNIYQNSQFL 180
CC	APPLICANT: Armistage, Richard J.	CC	140 FPGLYFIVCOLQFLVQCSNHSVDLFLQLLINSKIKQTLLVTVCSGVQSKNIYQNSQFL 199
CC	APPLICANT: Gruss, Hans-Jurgen	CC	181 LHYLVNSTISVRVDNFOYDNTNFPDLNVLVSFLYSSD 220
CC	TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30	CC	200 LHYLVNSTISVRVDNFOYDNTNFPDLNVLVSFLYSSD 239
CC	NUMBER OF SEQUENCES: 23	CC	RESULT 8
CC	CORRESPONDENCE ADDRESS:	CC	ID US-08-570-923-8 STANDARD; PRT: 234 AA.
CC	ADDRESSEE: Kathryn A. Seese, Immunex Corporation	CC	xxxxxx
CC	STREET: 51 University Street	CC	Sequence 8, Application US/08225989
CC	City: Seattle	CC	Patent No. 5480981
CC	STATE: Washington	CC	GENERAL INFORMATION:
CC	COUNTRY: USA	CC	APPLICANT: Goodwin, Raymond G.
CC	ZIP: 98101	CC	APPLICANT: Smith, Craig A.
CC	COMPUTER READABLE FORM:	CC	APPLICANT: Armistage, Richard J.
CC	MEDIUM TYPE: Floppy disk	CC	APPLICANT: Gruss, Hans-Jurgen
CC	COMPUTER: Apple Macintosh	CC	TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
CC		CC	NUMBER OF SEQUENCES: 23
CC		CC	CORRESPONDENCE ADDRESS:
CC		CC	ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC		CC	STREET: 51 University Street
CC		CC	City: Seattle
CC		CC	STATE: Washington
CC		CC	COUNTRY: USA
CC		CC	ZIP: 98101
CC		CC	COMPUTER READABLE FORM:
CC		CC	MEDIUM TYPE: Floppy disk
CC		CC	COMPUTER: Apple Macintosh

CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822

CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 234 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 234 AA; 26017 MW; 308679 CN;

CC Query Match 71.7%; Score 1232; DB 1; Length 234;
CC Best Local Similarity 70.0%; Pred. No. 4.21e-98;
CC Matches 168; Conservative 39; Mismatches 26; Indels 7; Gaps 3;

Db 1 MDPGLQALNGAPPDGTAMHVPGSVASHL-GT-----TSRSFYILTATLALCLVFTV 54
QY 1 MDPGLQALNGAPPDGTAMHVPGSVASHL-GT-----TSRSFYILTATLALCLVFTV 59

Db 55 ATIMLVQRTSDIPNSPNVPLKGNCSDELICILKRAPFKSWAYLOVAKHLNKTLS 114
QY 55 ATIMLVQRTSDIPNSPNVPLKGNCSDELICILKRAPFKSWAYLOVAKHLNKTLS 119

Db 115 WNKDGLHGVYQDGNLVTFQFGLYFIICQLQFLVCPNNSVDLKLLELLINKHIKQALV 174
QY 115 WNKDGLHGVYQDGNLVTFQFGLYFIICQLQFLVCPNNSVDLKLLELLINKHIKQALV 179

Db 175 TVCESGMQTKHYQNLQSFLLDLYQVNTTISVNVDFQYIDTFTFPLENVLSIFLYSNSD 234
QY 175 TVCESGMQTKHYQNLQSFLLDLYQVNTTISVNVDFQYIDTFTFPLENVLSIFLYSNSD 239

RESULT 9
ID US-08-580-014-8 STANDARD; PRT; 234 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
Sequence 8, Application US/08580014
Sequence 8, Application US/08580014
Patent No. 5753203
GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580,014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822

CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 234 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 234 AA; 26017 MW; 308679 CN;

CC Query Match 71.7%; Score 1232; DB 2; Length 234;
CC Best Local Similarity 70.0%; Pred. No. 4.21e-98;
CC Matches 168; Conservative 39; Mismatches 26; Indels 7; Gaps 3;

Db 1 MDPGLQALNGAPPDGTAMHVPGSVASHL-GT-----TSRSFYILTATLALCLVFTV 54
QY 1 MDPGLQALNGAPPDGTAMHVPGSVASHL-GT-----TSRSFYILTATLALCLVFTV 59

Db 55 ATIMLVQRTSDIPNSPNVPLKGNCSDELICILKRAPFKSWAYLOVAKHLNKTLS 114
QY 55 ATIMLVQRTSDIPNSPNVPLKGNCSDELICILKRAPFKSWAYLOVAKHLNKTLS 119

Db 115 WNKDGLHGVYQDGNLVTFQFGLYFIICQLQFLVCPNNSVDLKLLELLINKHIKQALV 174
QY 115 WNKDGLHGVYQDGNLVTFQFGLYFIICQLQFLVCPNNSVDLKLLELLINKHIKQALV 179

Db 175 TVCESGMQTKHYQNLQSFLLDLYQVNTTISVNVDFQYIDTFTFPLENVLSIFLYSNSD 234
QY 175 TVCESGMQTKHYQNLQSFLLDLYQVNTTISVNVDFQYIDTFTFPLENVLSIFLYSNSD 239

Db 1 MDPGLQALNGMAPPGDTAMHVPAAGSVASHL-GT-----TSRSYFYLTTATLALCLVFTV 54
QY 1 MEPGLQAGSCGAPSPDPAQVQPGSVASPWRSRPRSRYSFYLSTAL-VCLVAV 59
Db 55 ATIMLVVQRTDIPNSPDNVLPLKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLS 114
QY 60 AAILVLVQKQDSTPNTTEKAPLKGNCSEDLFTLKSTPSKRSWAYLQVSKHLNKTLS 119
Db 115 WNKDGIHLGVYQDGNLVIQPGFLYFIICQLQFLVQCPNNSVDLKLKLLINKHKKQALV 174
QY 120 WNEGTTHGLIYQDGNLVIQPGFLYFIICQLQFLVQCPNNSVDLKLKLLINKHKKQALV 179
Db 175 TVCESGMQTKHVTQNLQSFLLDYQVNTTISVNVDTFQYIDTSTFFLENVLSIFLYNSD 234
QY 180 TVCESGVQSNIVQNLQSFLLHYLVNSTISVRVDFQYVDTNFTPLDNVLSVFLYSSD 239
RESULT 10
ID US-08-570-923-23 STANDARD; PRT; 215 AA.
XX
AC xxxxxx
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DT
XX
DE Sequence 23, Application US/08570923
XX
CC Sequence 23, Application US/08570923
CC Patent No. 5677430
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Amitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172

CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 215 AA; 24151 MW; 261175 CN;
SQ
Query Match 69.2%; Score 1189; DB 1; Length 215;
Best Local Similarity 73.8%; Pred No. 3 09e-94;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;
Db 14 TTSRSYFYLTTATLALCLVFTVATIMVLVQRTDIPNSPDNVLKGGNCSEDLICILKR 73
QY 39 STSRYSFYLSTAL-VCLVAVAILVLVQKDKSTPNTTEKAPLKGNCSEDLFTLKLS 97
Db 74 APFKSWAYLQVAKHLNKTLSWKNKDGILHGVYQDGNLVIQPGFLYFIICQLQFLVQCP 133
QY 98 TPSKSWAYLQVSKHLNKTLSWKNKDGILHGVYQDGNLVIQPGFLYFIICQLQFLVQCS 157
Db 134 NNSVDLKLKLLINKHKKQALVTVCESGMQTKHVTQNLQSFLLDYQVNTTISVNVDTFQ 193
QY 158 NNSVDLKLKLLINKHKKQALVTVCESGMQTKHVTQNLQSFLLDYQVNTTISVNVDTFQ 193
Db 194 YIDTSTFFLENVLSIFLYNSD 215
QY 218 YVDNFTPLDNVLSVFLYSSD 239
RESULT 11
ID US-08-580-014-23 STANDARD; PRT; 215 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 23, Application US/08580014
XX
CC Sequence 23, Application US/08580014
CC Patent No. 5753203
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Amitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580,014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992

CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 215 AA; 24151 MW; 261175 CN;

Query Match 69.2%; Score 1189; DB 2; Length 215;
Best Local Similarity 73.8%; Pred. No. 3,09e-94;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;

Db 14 TTSRSYFYLTTATLALCLVFTVATIMVLVYQRTDSIPNSPDNVLKGGNCSEDLCLILKR 73
QY 39 STSRSYFYLSTTAL-VCLVAVAILLVVQKDDSTPNTTEKAPLKGNCSEDLFCTLKS 97

Db 74 APFKKSWAYLQVAKHLNKLKSNKGDILHGVRVYQDGNLVFIQFGLYFIICQLQFLVQCP 133
QY 98 TPSKKSWAYLQVSKHLNKLKSNWEDGTIHLIYQDGNLVFIQFGLYFIICQLQFLVQCS 157

Db 134 NNSVDLKLLELLINKHKQALVTVCESGMOTKHVYQNLQSLQFLDYLVQNTTISVNDTFQ 193
QY 158 NHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLQSLQFLHYLVQNTTISVRVDNFQ 217

Db 194 YDTSFTFPLENLSIFLYSNSD 215
QY 218 YVDNTFFPLDNVLSVFLYSSSD 239

RESULT 12
ID US-08-225-989-23 STANDARD; PRT; 215 AA.
XX xxxxxx
AC
XX
DE
DE Sequence 23, Application US/08225989
CC
CC Sequence 23, Application US/08225989
CC Patent No. 5480981
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5480981el Cytokine That Blinds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington

CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 215 AA; 24151 MW; 261175 CN;

Query Match 69.2%; Score 1189; DB 1; Length 215;
Best Local Similarity 73.8%; Pred. No. 3,09e-94;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;

Db 14 TTSRSYFYLTTATLALCLVFTVATIMVLVYQRTDSIPNSPDNVLKGGNCSEDLCLILKR 73
QY 39 STSRSYFYLSTTAL-VCLVAVAILLVVQKDDSTPNTTEKAPLKGNCSEDLFCTLKS 97

Db 74 APFKKSWAYLQVAKHLNKLKSNKGDILHGVRVYQDGNLVFIQFGLYFIICQLQFLVQCP 133
QY 98 TPSKKSWAYLQVSKHLNKLKSNWEDGTIHLIYQDGNLVFIQFGLYFIICQLQFLVQCS 157

Db 134 NNSVDLKLLELLINKHKQALVTVCESGMOTKHVYQNLQSLQFLDYLVQNTTISVNDTFQ 193
QY 158 NHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLQSLQFLHYLVQNTTISVRVDNFQ 217

Db 194 YDTSFTFPLENLSIFLYSNSD 215
QY 218 YVDNTFFPLDNVLSVFLYSSSD 239

RESULT 13
ID US-08-580-014-21 STANDARD; PRT; 130 AA.
XX xxxxxx
AC
XX
DT
XX
DE Sequence 21, Application US/08580014
XX

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CC Sequence 21, Application US/08580014
CC Patent No. 5753203
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580,014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 130 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein fragment
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC IMMEDIATE SOURCE:
CC CLONE: mUCD30 fragment (PRELIM)
CC SEQUENCE 130 AA; 14522 MW; 97051 CN;

Query Match 55.3%; Score 951; DB 2; Length 130;
Best Local Similarity 99.2%; Pred. No. 6,70e-73;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MGVQPGSVASPRWRSTSRYSFYLTALVCLVAVAILLVVYVKKDSPTNTEK 60
QY 20 MGVQPGSVASPRWRSTSRYSFYLTALVCLVAVAILLVVYVKKDSPTNTEK 79
Db 61 APLKGGNCSEDLFCTLKSTPSKSWAYLVQSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
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QY 80 APLKGGNCSEDLFCTLKSTPSKSWAYLVQSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 139
Db 121 FPGLYFIVCQ 130
QY 140 FPGLYFIVCQ 149

RESULT 14
ID US-08-225-989-21 STANDARD; PRT; 130 AA.
XX
AC xxxxxx
DT
XX
XX
DE
XX
XX Sequence 21, Application US/08225989
XX Sequence 21, Application US/08225989
CC Patent No. 5480981
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 130 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein fragment
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CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC IMMEDIATE SOURCE:
CC CLONE: muCD30 fragment (PRELIM)
SQ SEQUENCE 130 AA; 14522 MW; 97051 CN;

Query Match 55.3%; Score 951; DB 1; Length 130;
Best Local Similarity 99.2%; Pred. No. 6.70e-73;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MQVQGSVASPWRSTRPWRSTRSYFLSTALVCLVAVAILLVVQKKDSTPNTTEK 60
QY 20 MQVQGSVASPWRSTRPWRSTRSYFLSTALVCLVAVAILLVVQKKDSTPNTTEK 79
Db 61 APLKGGNCSEDLFTLKSTPSKSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
QY 80 APLKGGNCSEDLFTLKSTPSKSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 139
Db 121 FPGLYFIVCQ 130
QY 140 FPGLYFIVCQ 149

RESULT 15
ID US-08-570-923-21 STANDARD; PRT; 130 AA.
XX xxxxxx
AC
XX
DT
XX
DE Sequence 21, Application US/08570923
CC Sequence 21, Application US/08570923
CC Patent No. 5677430
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Blinds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 130 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein fragment
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC IMMEDIATE SOURCE:
CC CLONE: muCD30 fragment (PRELIM)
SQ SEQUENCE 130 AA; 14522 MW; 97051 CN;

Query Match 55.3%; Score 951; DB 1; Length 130;
Best Local Similarity 99.2%; Pred. No. 6.70e-73;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MQVQGSVASPWRSTRPWRSTRSYFLSTALVCLVAVAILLVVQKKDSTPNTTEK 60
QY 20 MQVQGSVASPWRSTRPWRSTRSYFLSTALVCLVAVAILLVVQKKDSTPNTTEK 79
Db 61 APLKGGNCSEDLFTLKSTPSKSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
QY 80 APLKGGNCSEDLFTLKSTPSKSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 139
Db 121 FPGLYFIVCQ 130
QY 140 FPGLYFIVCQ 149

Search completed: Fri Aug 13 16:39:04 1999
Job time : 20 secs.

W P E L A

(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Aug 13 16:36:30 1999; MasPar time 11.92 Seconds
Tabular output not generated. 803.290 Million cell updates/sec

Title: >US-09-079-785-6
Description: (1-239) from US09079785.pep
Perfect Score: 1719
Sequence: 1 MEPGLQAGSGCAPSPDPAM.....DNTFPLDNLVFLYSSSD 239

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 45.006; Variance 89.087; scale 0.505

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	1719	100.0	239	2	B40710	CD30 ligand - mouse	0.00e+00
2	1232	71.7	234	2	A40710	CD30 ligand - human	6.90e-226
3	117	6.8	498	2	S52570	phosphoprotein phosph	2.67e-03
4	115	6.7	560	2	D59649	probable long-chain-f	5.09e-03
5	113	6.6	279	2	A53062	Fas ligand - mouse	9.64e-03
6	111	6.5	499	2	A53346	phosphoprotein phosph	1.81e-02
7	109	6.3	397	2	B27496	proteinase inhibitor	3.39e-02
8	104	6.1	619	2	S54636	probable membrane pro	1.57e-01
9	103	6.0	693	2	S49228	sodium-dependent phos	2.13e-01
10	101	5.9	278	2	A49266	fas ligand - rat	3.86e-01
11	99	5.8	249	2	G64081	fuc operon regulatory	6.96e-01
12	99	5.8	259	2	C36819	Cil protein - rabbit	6.96e-01
13	100	5.8	598	2	S51456	probable membrane pro	5.19e-01
14	98	5.7	397	2	I48717	proteinase inhibitor	9.32e-01
15	97	5.6	560	2	S27874	steroid hormone recep	1.25e-00
16	96	5.6	4910	2	S64942	probable membrane pro	1.66e+00
17	94	5.5	281	2	I38707	Fas ligand - human	2.93e+00
18	94	5.5	434	2	T02407	heme A farnesyltransf	2.93e+00
19	95	5.5	445	2	S58282	ATDP-glucose 4-6-dehy	2.21e+00
20	94	5.5	469	2	T01579	heme A:farnesyltransf	2.93e+00
21	94	5.5	476	2	A48664	toxin synthesis trans	2.93e+00
22	94	5.5	1770	2	A71517	hypothetical protein	2.93e+00
23	92	5.4	155	2	G59987	hypothetical protein	5.13e+00

24	92	5.4	197	2	JH0309	tumor necrosis factor	5.13e+00
25	93	5.4	220	2	H70568	hypothetical protein	3.88e+00
26	92	5.4	314	2	S31402	3-methylcatechol 2,3-	5.13e+00
27	92	5.4	407	2	J01654	SFR1 protein - human	5.13e+00
28	93	5.4	418	2	S11678	cyclin A - African cl	3.88e+00
29	93	5.4	575	2	G59834	transporter binding P	3.88e+00
30	93	5.4	397	2	A27496	glia-derived nexin I	6.76e+00
31	91	5.3	412	2	S66925	hypothetical protein	6.76e+00
32	91	5.3	427	2	F64084	3-deoxy-D-manno-octul	6.76e+00
33	91	5.3	1524	2	S68553	surface layer protein	6.76e+00
34	91	5.3	2787	2	S45416	TEL1 protein - yeast	6.76e+00
35	90	5.2	249	2	S78186	H+-transporting ATP s	8.88e+00
36	90	5.2	379	2	S67856	Gumg protein - Xantho	8.88e+00
37	89	5.2	388	2	B64459	Na+/H+-exchanging pro	1.17e+01
38	89	5.2	416	1	A31959	lysosome-associated m	1.17e+01
39	89	5.2	428	1	B32804	GTP-binding protein o	1.17e+01
40	90	5.2	568	2	JC5629	Muellerian-inhibiting	8.88e+00
41	90	5.2	746	2	S44792	F09G8.8 protein - Cae	8.88e+00
42	90	5.2	779	2	S36111	osteoblast-specific f	8.88e+00
43	90	5.2	836	2	S36110	osteoblast-specific f	8.88e+00
44	89	5.2	836	2	J50248	ATP-binding cassette	1.17e+01
45	89	5.2	1636	2	S60403	probable membrane pro	1.17e+01

ALIGNMENTS

RESULT 1
ENTRY B40710 #type complete
TITLE CD30 ligand - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-1999

ACCESSIONS B40710
REFERENCE A40710

#authors Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, G.R.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Grabstein, K.H.; Gliniak, B.; McAllister, I.B.; Fanslow, W.; Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, R.J.

#journal Cell (1993) 73:1349-1360
#title CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand defines an emerging family of cytokines with homology to TNF.

#cross-references MIMD:93313964
#accession B40710

##status preliminary
##molecule_type mRNA
##residues 1-239 #label SMI
##cross-references GB:L05754; NID:g349288; PID:g349289
#KEYWORDS cytokine receptor; membrane protein; surface antigen
#length 239 #molecular-weight 26519 #checksum 3403

SUMMARY

Db	1	MEPGLQAGSGCAPSPDPAMQVPGSVASPRWRSTRPWRSTRSRFYLTALVCLVAVA	60
Qy	1	MEPGLQAGSGCAPSPDPAMQVPGSVASPRWRSTRPWRSTRSRFYLTALVCLVAVA	60
Db	61	IILVLVQKSDSTNTTEKAPLKGNCSEDLFCILKSTPSKSWAYLOVSHLNTKLSW	120
Qy	61	IILVLVQKSDSTNTTEKAPLKGNCSEDLFCILKSTPSKSWAYLOVSHLNTKLSW	120
Db	121	NEDGTIHLIYQDGNLIVQFPGFYVCQLQFLVQCSNHSVDLTLOLLINSKIKQTIVT	180
Qy	121	NEDGTIHLIYQDGNLIVQFPGFYVCQLQFLVQCSNHSVDLTLOLLINSKIKQTIVT	180
Db	181	VCSGVQSKNIYQNLQSLFLLHYLQVNSTISVRVDNFQVDNTFPDLNVLVFLYSSSD	239
Qy	181	VCSGVQSKNIYQNLQSLFLLHYLQVNSTISVRVDNFQVDNTFPDLNVLVFLYSSSD	239

```

S.; Zetterberg, A.
Biochem. Biophys. Res. Commun. (1996) 218:514-517
Chromosomal localization and 5' sequence of the human protein
serine/threonine phosphatase 5', gene.
#accession PC4136
#molecule_type mRNA
#residues 1-37 #label XUX
##cross-references EMBL:X92121; NID:g1177477; PID:e05526; PID:g1177478
##experimental_source fetal brain
GENETICS
#gene GDB:PPP5C; PPP5; PP5
##cross-references GDB:136857
#map_position 19q13.3-19q13.3
FUNCTION
#description catalyzes the hydrolytic dephosphorylation of
protein-phosphoserine and protein-psothreo-nine
plays a role in the regulation of RNA synthesis and mitosis
CLASSIFICATION
#superfamily phosphoprotein phosphatase homology;
phosphoesterase core homology; tetratricopeptide repeat
homology
KEYWORDS
iron; nucleus; phosphoric monoester hydrolase; zinc
FEATURE
68-61 #domain tetratricopeptide repeat homology #label TT1\
62-95 #domain tetratricopeptide repeat homology #label TT2\
96-129 #domain tetratricopeptide repeat homology #label TT3\
204-467 #domain phosphoprotein phosphatase homology #label PPP\
236-305 #domain phosphoesterase core homology #label PPC\
242,244,271 #binding_site iron (Asp, His, Asp) #status predicted\
271,303,352,426 #binding_site zinc (Asp, Asn, His, His) #status
predicted\
274,304,450 #active_site Asp, His, Tyr #status predicted\
275,399 #binding_site substrate phosphate (Arg) #status
predicted\
SUMMARY
#length 498 #molecular-weight 56820 #checksum 5353
Query Match 6.8%; Score 117; DB 2; Length 498;
Best Local Similarity 23.9%; Pred. NO. 2.67e-03;
Matches 21; Conservative 29; Mismatches 32; Indels 6; Gaps 6;
Db 208 CAYILYQ-VKEVLS-KLSTVTETLKETEKITVC-GPTHGQ-FYDLNIFELNGLPST 263
| :||| | : ||:::|K||| :||:| :||:| :||:| :||:| :||:|
QY 148 CQLQFLQCNSHSDLFLLQDINSKIQTUVTVCSCVKNIQNLSQFLLHYLQVNS 207
| :||| | : ||:::|K||| :||:| :||:| :||:| :||:| :||:|
Db 264 NPXI-FNG-DPVDGRGSFSEVILTFFG 289
: :||| :||:| :||:| :||:| :||:| :||:| :||:|
QY 208 TISRVDFNQYVDNTPLDNVLVSFLY 235
: :||| :||:| :||:| :||:| :||:| :||:| :||:|
RESULT 4
ENTRY #type complete
TITLE probable long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) lcfa
ORGANISM - Bacillus subtilis
#format_name Bacillus subtilis
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
05-Feb-1999
D69649
D69649
A69580
AUTHORS
Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devigne, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Haech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klagerl-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.;

```

Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwollik, S.; Prescott, A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serrori, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenecker, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

#journal Nature (1997) 390:249-256
#title The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

#cross-references MUID:96044033
#accession D69649
#status preliminary; nucleic acid sequence not shown; translation not shown

##molecule_type DNA
##residues 1-560 ##label KUN
##cross-references GB:Z99118; GB:AL009126; NID:G2635200; PID:el184105; PID:G2635321

##experimental_source strain 168

GENETICS lcfa

CLASSIFICATION #superfamily acetate--CoA ligase homology
KEYWORDS acid-thiol ligase
FEATURE #length 560 #molecular-weight 62691 #checksum 4760
SUMMARY

Query Match 6.7%; Score 115; DB 2; Length 560;
Best Local Similarity 27.3%; Pred. No. 5.09e-03;
Matches 27; Conservative 28; Mismatches 38; Indels 6; Gaps 6;

Db 93 GVLP-AGGIVQTNPLY-TEHELYQLRDAQVSVITLIDLLFPRAIKMTLSIVDQILIT 150
Qy 128 GLIYODGNLIVFPGFLVFCOLOFLVQCSNHSVDLTQLLINSKIRKQTLTVCSGVQ 187

Db 151 SVKDYLPFPKNIL-Y-PLTQKQKVID-FDKTANTHTFA 186
Qy 188 SKNIYQNLSQLHYLQVNSISVRVDNFQ-YVDNTFP 225

RESULT 5
ENTRY Fas ligand - mouse
TITLE #type complete
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997
ACCESSIONS A53062
REFERENCE A53062
#authors Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Negata, S.
#journal Cell (1994) 76:969-976
#title Generalized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand.
#cross-references MUID:94185175
#accession A53062
#status preliminary
#molecule_type mRNA
##residues 1-279 ##label TAK
##cross-references GB:U06948; NID:G473564; PID:G473565
SUMMARY #length 279 #molecular-weight 31442 #checksum 3291

Query Match 6.6%; Score 113; DB 2; Length 279;
Best Local Similarity 32.3%; Pred. No. 9.64e-03;
Matches 20; Conservative 14; Mismatches 24; Indels 4; Gaps 3;

Db 145 AHLTGNPHSRSPLEWEDTYGTALISGVYKKGGLVINETGLYFYVSKYVFRQSCNNQP 204
Qy 105 AYLOYSKHLNNTKLSWNE-DGT--IHGLIYODGNLIVFPGFLVFCOLOFLVQ-CSNHS 160

Db 205 LN 206
Qy 161 VD 162

RESULT 6
ENTRY A55346 #type complete
TITLE phosphoprotein phosphatase (EC 3.1.3.16) PPT - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-1999
ACCESSIONS A55346
REFERENCE A55346
#authors Becker, W.; Kentrup, H.; Klumpp, S.; Schultz, J.E.; Joost, H.G.
#journal J. Biol. Chem. (1994) 269:22586-22592
#title Molecular cloning of a protein serine/threonine phosphatase containing a putative regulatory tetratricopeptide repeat domain.
#cross-references MUID:94357899
#accession A55346
#status preliminary
##molecule_type mRNA
##residues 1-499 ##label BEC
##cross-references GB:X77237
#note authors translated the codon AAG for residue 53 as Gln, and GTA for residue 496 as Leu

CLASSIFICATION #superfamily phosphoprotein phosphatase homology;
KEYWORDS phosphoesterase core homology; tetratricopeptide repeat homology
phosphoric monoester hydrolase

FEATURE #domain tetratricopeptide repeat homology #label TT1\
28-61 #domain tetratricopeptide repeat homology #label TT2\
62-95 #domain tetratricopeptide repeat homology #label TT3\
96-129 #domain phosphoprotein phosphatase homology #label PPP\
204-468 #domain phosphoesterase core homology #label PEC
236-305 #length 499 #molecular-weight 56902 #checksum 8503
SUMMARY

Query Match 6.5%; Score 111; DB 2; Length 499;
Best Local Similarity 25.8%; Pred. No. 1.81e-02;
Matches 23; Conservative 28; Mismatches 30; Indels 8; Gaps 8;

Db 208 CAYQILVQ-VKE-V-LCKLSTLVETLRETEKITVC-GDTHGQ-FYDLNIFELNGLPSE 262
Qy 148 COLOFLVQCSNHSVDL-TQLLINSKIRKQTLTVCSGVQSKNIYQNLSQLHYLQVN 206

Db 263 TNPYT-FNG-DFVDRGFSFSEVILTLCGF 289
Qy 207 STISVRVDNFQYVDNTFPDLNVLVSFLY 235

RESULT 7
ENTRY B27496 #type fragment
TITLE proteinase inhibitor nexin 1 precursor - rat (fragment)
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 05-Dec-1998
ACCESSIONS B27496; A34538; A42351; B42351; C42351
REFERENCE A90519
#authors Sommer, J.; Gloor, S.M.; Rovelli, G.F.; Hofsteenge, J.; Nick, H.; Weier, R.; Monard, D.
#journal Biochemistry (1987) 26:6407-6410
#title CDNA sequence coding for a rat glia-derived nexin and its

9


```

ACCESSIONS      A49266
REFERENCE        A49266
#authors        Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
#journal        Cell (1993) 75:1169-1178
#title          Molecular cloning and expression of the Fas ligand, a novel
#               member of the tumor necrosis factor family.
#cross-references MUID:94084792
#accession      A49266
#status         preliminary
#molecule_type mRNA
#residues       1-278 #label SUD
#cross-references GB:U03470; NID:9440178; PID:g440179
KEYWORDS         glycoprotein; transmembrane protein
SUMMARY          #length 278 #molecular-weight 31140 #checksum 9586

Query Match      5.9%; Score 101; DB 2; Length 278;
Best Local Similarity 33.3%; Pred. No. 3.86e-01;
Matches 16; Conservative 13; Mismatches 15; Indels 4; Gaps 3;

Db 157 LEWEDTGTALISGVKKYKGGVLINAGLYFYVSKYFVGOSCSOPL 204
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Qy 118 LSWNED-GT--IHGLIYQDGNLIVQFPGLIYFIVCOLQLVQ-CSNSHV 161
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 11
ENTRY   G64081 #type complete
TITLE   fuc operon regulatory protein homolog - Haemophilus
        influenzae (strain Rd KW20)
ORGANISM #formal_name Haemophilus influenzae
DATE      18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
        24-Oct-1997

ACCESSIONS G64081
REFERENCE   G64000
#authors    Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
            Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
            Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
            Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
            Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
            J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
            M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
            D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
            J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
            Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal    Science (1995) 269:496-512
#title      Whole-genome random sequencing and assembly of Haemophilus
            influenzae Rd.
#cross-references MUID:95350630
#accession  G64081
#status     nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues   1-249 #label TIGR
#cross-references GB:U32744; GB:L42023; NID:g1573608; PID:g1573609;
            TIGR:HI0615
SUMMARY      #length 249 #molecular-weight 28163 #checksum 2069

Query Match      5.8%; Score 99; DB 2; Length 249;
Best Local Similarity 19.6%; Pred. No. 6.96e-01;
Matches 21; Conservative 35; Mismatches 46; Indels 5; Gaps 5;

Db 64 SFFQTRKHINATA-KRHTAOKALDLLYENAVIGLDASTSWYFAYLMP-DIPCTVVTNSM 121
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Qy 105 AYLVQSRHLNKLKSWNEDGTHGLIYQDGNLIVQFPGLIYFIVCOLQLVQCSNHSVDL 163
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

Db 122 FNIALVN-KSNKVTIVGVYSARYEAFYGPLSEYLLQRLHINFSV 167
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Qy 164 -TLQLLINSKIKKOTLVTCVSGVQSKNIYQNLQFLLHYLQVNSTI 209
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 12
ENTRY   C36819 #type complete
TITLE   C11 protein - rabbit fibroma virus
ORGANISM #formal_name rabbit fibroma virus, Shope fibroma virus
DATE      23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change

```

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21-Aug-1998
ACCESSIONS      C36819
REFERENCE        A41700
#authors        Straver, D.S.; Jerng, H.H.; O'Connor, K.
#journal        Virology (1991) 185:585-595
#title          Sequence and analysis of a portion of the genomes of Shope
#               fibroma virus and malignant rabbit fibroma virus that is
#               important for viral replication in lymphocytes.
#accession      C36819
#status         translation not shown
#molecule_type DNA
#residues       1-259 #label STR
#cross-references GB:M32743
CLASSIFICATION  #superfamily vaccinia virus D10R protein; mutT domain
                homology
FEATURE         #domain mutT domain homology #label MUTT
123-157
SUMMARY          #length 259 #molecular-weight 30411 #checksum 5504

Query Match      5.8%; Score 99; DB 2; Length 259;
Best Local Similarity 28.3%; Pred. No. 6.96e-01;
Matches 15; Conservative 19; Mismatches 16; Indels 3; Gaps 3;

Db 147 EINDSKDIYD-SRFFVH-LFIEDLLSNRIYETILFLGKTLTSHIELNLF 197
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Qy 183 ESGVQSKNIYQNLQFLLHYLQVNSTISVRV-DNEQYVDNTFFPLDNLVLSVL 234
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 13
ENTRY   S51456 #type complete
TITLE   probable membrane protein YLR237w - yeast (Saccharomyces
        cerevisiae)
ALTERNATE_NAMES hypothetical protein L8083.2
ORGANISM #formal_name Saccharomyces cerevisiae
DATE      23-Feb-1995 #sequence_revision 12-May-1995 #text_change
        06-Feb-1998

ACCESSIONS      S51456
REFERENCE        S51443
#authors        Hallsworth, K.
#submission     Submitted to the EMBL Data Library, December 1994
#description     The sequence of S. cerevisiae cosmid 8083.
#accession      S51456
#molecule_type DNA
#residues       1-598 #label HAL
#cross-references EMBL:U19027; NID:g609363; PID:g609365; MIPS:YLR237w
GENETICS
#gene          SGD:THI7
#cross-references SGD:S0004227; MIPS:YLR237w
#map_position  12R
KEYWORDS        transmembrane protein
FEATURE         #domain transmembrane #status predicted #label TM1\
116-132         #domain transmembrane #status predicted #label TM2\
174-190         #domain transmembrane #status predicted #label TM3\
199-215         #domain transmembrane #status predicted #label TM4\
280-296         #domain transmembrane #status predicted #label TM5\
398-414         #domain transmembrane #status predicted #label TM6\
485-501         #domain transmembrane #status predicted #label TM7\
SUMMARY          #length 598 #molecular-weight 66903 #checksum 8385

Query Match      5.8%; Score 100; DB 2; Length 598;
Best Local Similarity 30.2%; Pred. No. 5.19e-01;
Matches 19; Conservative 16; Mismatches 25; Indels 3; Gaps 3;

Db 334 FGLSFLVLSOMSYTISNCGFASGMDLAGLLPKYVDIKRGALFAACVSWACLFWNFYNSSS 393
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Qy 140 FPLGFIYVQLOFLV-QCS-NHSVDLTQLLINSIKKOTLVTCES-GVQSKNIYQNL 196
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

Db 394 TFL 396
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Qy 197 QFL 199
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |

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```
RESULT 14
ENTRY   #type complete
TITLE   proteinase inhibitor nexin I precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE    02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS 05-Dec-1998
REFERENCE  I48717; S70772; S35731
#authors  Vassalli, J.D.; Huarte, J.; Bosco, D.; Sappino, A.P.;
           Sappino, N.; Velardi, A.; Wohlwend, A.; Erno, H.; Monard,
           D.; Belin, D.
#journal  EMBO J. (1993) 12:1871-1878
#title    Protease-nexin I as an androgen-dependent secretory product
           of the murine seminal vesicle.
#cross-references EMBL:93259128
#accession I48717
#status    preliminary; translated from GB/EMBL/DDBJ
#molecule_type mRNA
#residues  1-397 #label RES
#cross-references EMBL:X70296; NID:g551064; PID:g551065
#accession S70772
#status    nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues  1-86 #label VAS
#cross-references EMBL:X70946; NID:g57930; PID:g57931
#note      the nucleotide sequence was submitted to the EMBL Data
           Library, February 1993
GENETICS
#gene      PN-1
CLASSIFICATION #superfamily antithrombin III
KEYWORDS     serine proteinase inhibitor
FEATURE
1-19
20-397
SUMMARY      #length 397 #molecular-weight 44207 #checksum 3957
Query Match 5.7%; Score 98; DB 2; Length 397;
Best Local Similarity 28.2%; Pred. No. 9.32e-01;
Matches 31; Conservative 26; Mismatches 49; Indels 4; Gaps 4;
Db 285 VPKRMVLVLPKFTAVQTDKPLKALGITE-MFEPKANKFTKTRSESHVSHILQKAK 343
QY 59 VAILVLVYQKKDSTNTTEKAPLKGNGCEDLCTLKSTPSKSWA-YLQVSKHLNNTK 117
Db 344 IEVSEGGTKASRA-TTALLIARSSPPWFIV-DRPFLFSIRHNPTGAILFL 391
QY 118 LSWNEDGTIHLIYQDGNLIVQPGLYFIVCQLQLVQCSNHSVDLTQL 167

RESULT 15
ENTRY   #type complete
TITLE   steroid hormone receptor homolog LRH-1 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE    17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
ACCESSIONS 10-Oct-1997
REFERENCE  S27874
#authors  Tugwood, J.D.; Issemann, I.; Green, S.
#submission submitted to the EMBL Data Library, February 1992
#description LRH-1: A nuclear hormone receptor active in the absence of
           exogenous ligands.
#accession S27874
#molecule_type mRNA
#residues  1-560 #label TUG
#cross-references EMBL:M81385; NID:g198872; PID:g198875
FUNCTION
#description transcription regulation; probably a steroid hormone receptor
CLASSIFICATION #superfamily steroid hormone receptor Ad4BP; erba
transforming protein homology
KEYWORDS     DNA binding; nucleus; steroid hormone receptor; transcription
           factor; zinc finger
FEATURE
```

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105-478      #domain erba transforming protein homology #label ERBA\
107-127      #region zinc finger CCCC motif\
143-167      #region zinc finger CCCC motif\
SUMMARY      #length 560 #molecular-weight 64020 #checksum 4722
Query Match 5.6%; Score 97; DB 2; Length 560;
Best Local Similarity 22.7%; Pred. No. 1.25e+00;
Matches 27; Conservative 38; Mismatches 44; Indels 10; Gaps 7;
Db 423 FLYTGEHVDYSTIISHTEVAFNNLLSLAQELVVRLSQFDQREFVC-LKELVLFSSDVK 481
QY 106 YLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIVQPGLYF----IVCQLQLVQCSNHSV 161
Db 482 NLENLQL-VEG-VOEQVNAALLDYVCNYPQOTEKFGQLLR-LPEIRAIKQAEADLY 537
QY 162 DL-TLQLLINSKIKQTLVTVCESGV-QSKNIYQNLQSLHLHYLQVNSTISVRVDNFOY 218
Search completed: Fri Aug 13 16:36:51 1999
Job time : 21 secs.
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M P S R E F L

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:37:07 1999; MasPar time 8.30 Seconds
Tabular output not generated. 814.080 Million cell updates/sec

Title: >US-09-079-785-6
Description: (1-239) from US09079785.pep
Perfect Score: 1719
Sequence: 1 MEPLGQAGSCGAPSPDPAM.....DTNFPDLNVLVFLYSSSD 239
Scoring table: PAM 150
Gap 11
Searched: 77977 seqs, 28268293 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot37
1:swissprot
Statistics: Mean 46.034; Variance 78.117; scale 0.589
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	1719	100.0	239	1	CD3L_MOUSE CD30 LIGAND (CD30-L).	0.00e+00	
2	1232	71.7	234	1	CD3L_HUMAN CD30 LIGAND (CD30-L) (3.69e+263	
3	117	6.8	499	1	PPP5_HUMAN SERINE/THREONINE PROTE	2.50e-04	
4	115	6.7	560	1	LCFA_BACSU LONG-CHAIN-FATTY-ACID-	5.23e-04	
5	113	6.6	279	1	FASL_MOUSE FAS ANTIGEN LIGAND.	1.09e-03	
6	111	6.5	499	1	PPP5_MOUSE SERINE/THREONINE PROTE	2.24e-03	
7	109	6.3	397	1	GDN_MOUSE GLIA DERIVED NEXIN PRE	4.58e-03	
8	104	6.1	260	1	VD10_SFVKA PROTEIN D10.	2.63e-02	
9	101	5.9	278	1	FASL_MOUSE FAS ANTIGEN LIGAND.	7.33e-02	
10	99	5.8	249	1	FUCR_HAEIN L-FUCOSE OPERON ACTIVA	1.43e-01	
11	100	5.8	598	1	TH17_YEAST THIAMINE TRANSPORTER.	1.03e-01	
12	98	5.7	397	1	GDN_MOUSE ALPHA-1-FETOPROTEIN TR	2.00e-01	
13	97	5.6	499	1	FTF_MOUSE ALPHA-1-FETOPROTEIN TR	5.32e-01	
14	95	5.5	233	1	TNFA_TRIVU TUMOR NECROSIS FACTOR	5.32e-01	
15	94	5.5	281	1	FASL_HUMAN FAS ANTIGEN LIGAND (AP	5.32e-01	
16	95	5.5	773	1	LI19_DRONE LIN-19 HOMOLOG PROTEIN	5.32e-01	
17	92	5.4	197	1	TNFB_RABIT LYMPHOTOXIN-ALPHA PREC	1.38e+00	
18	93	5.4	418	1	CGAL_XENLA U10 PROTEIN.	1.01e+00	
19	92	5.4	436	1	VU10_HSV6U U10 PROTEIN.	1.01e+00	
20	93	5.4	1202	1	YE01_SCHPO HYPOTHETICAL 138.5 KD	1.01e+00	
21	91	5.3	427	1	KDTA_HAEIN 3-DEOXY-D-MANNO-OCTULO	1.89e+00	
22	91	5.3	2787	1	TELMER_LENGTH REGULAT	1.89e+00	
23	90	5.2	233	1	TNFA_MACFA TUMOR NECROSIS FACTOR	2.58e+00	

24	89	5.2	375	1	GM12_SCHPO ALPHA-1.2-GALACTOSYLTR	3.50e+00
25	89	5.2	416	1	LMPI_HUMAN LYOSOME-ASSOCIATED ME	3.50e+00
26	89	5.2	427	1	7SBG_SOYBN BASIC 7S GLOBULIN PREC	3.50e+00
27	89	5.2	428	1	OBG_BACSU SPOOB-ASSOCIATED GTP-B	3.50e+00
28	89	5.2	599	1	THIY_YEAST PUTATIVE THIAMINE TRAN	3.50e+00
29	90	5.2	746	1	YLS8_CAEEL HYPOTHETICAL 83.6 KD P	2.58e+00
30	89	5.2	1156	1	JAK1_CYPCA TYROSINE-PROTEIN KINAS	3.50e+00
31	89	5.2	1191	1	TOP2_ASFM2 DNA TOPOISOMERASE II (3.50e+00
32	89	5.2	1636	1	YN37_YEAST HYPOTHETICAL 186.8 KD	3.50e+00
33	88	5.1	303	1	YLID_ECOLI HYPOTHETICAL ABC TRANS	4.75e+00
34	88	5.1	349	1	GBT1_MOUSE GUANINE NUCLEOTIDE-BIN	4.75e+00
35	88	5.1	349	1	GBT1_CANFA GUANINE NUCLEOTIDE-BIN	4.75e+00
36	87	5.1	349	1	GBT1_BOVIN GUANINE NUCLEOTIDE-BIN	6.42e+00
37	88	5.1	351	1	Y239_METJA HYPOTHETICAL PROTEIN M	4.75e+00
38	88	5.1	353	1	GBT2_MOUSE GUANINE NUCLEOTIDE-BIN	4.75e+00
39	88	5.1	353	1	GBT2_BOVIN GUANINE NUCLEOTIDE-BIN	4.75e+00
40	87	5.1	500	1	FTF_HUMAN ALPHA-1-FETOPROTEIN TR	6.42e+00
41	88	5.1	527	1	NU2M_ACACA NADH-UBIQUINONE OXIDOR	4.75e+00
42	88	5.1	585	1	DCE2_PIG GLUTAMATE DECARBOXYLAS	4.75e+00
43	88	5.1	585	1	DCE2_RAT GLUTAMATE DECARBOXYLAS	4.75e+00
44	88	5.1	769	1	SWI6_KLJLA REGULATORY PROTEIN SWI	4.75e+00
45	87	5.1	1580	1	SUR_FUMAN SULFONYLUREA RECEPTOR.	6.42e+00

ALIGNMENTS

RESULT 1
ID CD3L_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CD30 LIGAND (CD30-L).
GN CD30LG OR CD30L.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-T-CELL;
RX MEDLINE; 93313964.
RA SMITH C.A., GRUENSS H.-J., DAVIS T., ANDERSON D., FARRAH T.,
BAKER E., SUTHERLAND G.R., BRANNAN C.I., COPELAND N.G., JENKINS N.A.,
GRABSTEIN K.H., GLINKA B., MCALISTER I.B., FANSLON W., ALDERSON M.,
FALK B., GIMPEL S., GILLIS S., DIN W.S., GOODWIN R.G., ARMITAGE R.J.;
RT CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
ligand defines an emerging family of cytokines with homology to
TNF".
RL CELL 73:1349-1360(1993).
CC -1- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
T CELLS.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
CC EMBL; L09754; G349289; -
CC PIR; B40710; B40710.
CC MGD; MGI:88328; CD30L.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PSS0049; TNF_2; 1.
CC PFAM; PF00229; TNF; 1.
CC CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
CC DOMAIN 1 43
CC TRANSNM 44 67
CC DOMAIN 68 239
CC CARBOHYD 75
CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CC EXTRACELLULAR (POTENTIAL).
CC POTENTIAL.

RESOLUT	PP5_HUMAN	STANDARD;	PRT;	499 AA.
ID	PP5_HUMAN	STANDARD;	PRT;	499 AA.
AC	PS3041;	Q16722;		
DT	01-OCT-1996	(REL. 34, CREATED)		
DT	01-OCT-1996	(REL. 34, LAST SEQUENCE UPDATE)		
DT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)		
DE	SERINE/THREONINE PROTEIN PHOSPHATASE 5	(EC 3.1.3.16) (PP5) (PROTEIN		
DE	PHOSPHATASE T) (PP-T) (PPT).			
GN	PPP5C OR PPP5.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA;	CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;		
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.			
RN	[1]			
RP	SEQUENCE OF 7-499 FROM N.A.			
RX	MEDLINE; 95009829.			
RA	CHEN M.X., MCPARTLIN A.E., BROWN L., CHEN Y.H., BARKER H.M.,			
RA	COHEN P.T.W.;			
RT	"A novel human protein serine/threonine phosphatase, which possesses			
RT	four tetraatricopeptide repeat motifs and localizes to the nucleus.";			
RT	EMBO J. 13:4278-4290(1994).			
RN	[2]			
RP	SEQUENCE OF 9-499 FROM N.A.			
RC	TISSUE=FETAL BRAIN;			
RX	MEDLINE; 96115607.			
RA	YONG W.H., DEKI K., CHOU D., REEVES S.A., VON DETMLING A.,			
RA	GUSELLA J.F., MOHREWEISER H.W., BUCKLER A.J., LOUIS D.N.;			
RT	"Cloning of a highly conserved human protein serine-threonine			
RT	phosphatase gene from the glioma candidate region on chromosome			
RT	19q13.3.";			
RT	GENOMICS 29:533-536(1995).			
RN	[3]			
RP	SEQUENCE OF 1-37 FROM N.A.			
RC	TISSUE=FETAL BRAIN;			
RX	MEDLINE; 96144708.			
RA	XU X., LAGERCRANTZ J., ZICKERT P., BAJALICA-LAGERCRANTZ S.,			
RA	ZETTERBERG A.;			
RT	"Chromosomal localization and 5' sequence of the human protein			
RT	serine/threonine phosphatase 5' gene.";			
RT	BIOCHEM. BIOPHYS. RES. COMMUN. 218:514-517(1996).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS) OF 19-177.			
RX	MEDLINE; 98151343.			
RA	DAS A.K., COHEN P.W., BARFORD D.;			
RT	"The structure of the tetraatricopeptide repeats of protein			

[illegible]

```
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DE 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1).
GN P17 OR PN1.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88107544.
RA SOMMER J., GLOOR S.M., ROVELLI G.F., HOFSTEENGE J., NICK H.,
RA MEIER R., MONARD D.;
RT "cDNA sequence coding for a rat glia-derived nexin and its homology
to members of the serpin superfamily.";
RL BIOCHEMISTRY 26:6407-6410(1987).
CC -1- FUNCTION: THIS GLYCOPROTEIN PROMOTES NEURITE EXTENSION AND IS A
SERINE PROTEASE INHIBITOR WITH ACTIVITY TOWARD THROMBIN, TRYPSIN,
AND UROKINASE. BINDS HEPARIN.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC -----
DR EMBL; M17784; G204284; .
DR PIR; B27496; B27496.
DR PROSITE; PS00284; SERPIN; 1.
DR PFAM; PF00079; serpin; 1.
DR HSP; P05619; IHLE.
KW SERINE PROTEASE INHIBITOR; SERPIN; HEPARIN-BINDING; NEURONE;
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 397 GLIA DERIVED NEXIN.
FT CARBOHYD 159 159 POTENTIAL.
FT ACT_SITE 364 365 REACTIVE BOND (POTENTIAL).
SQ SEQUENCE 397 AA; 44063 MW; D79E9B21 CRC32;

Query Match 6.3%; Score 109; DB 1; Length 397;
Best Local Similarity 30.18; Pred. No. 4.58e-03;
Matches 31; Conservative 26; Mismatches 41; Indels 5; Gaps 5;

Db 285 VPKRMOLVLPKFTALQTLDEPLKALGITE-MPEPSKANFAKITRSESILVSHILOKAK 343
QY 59 VAILVLVQKDKSTPNTTEKAPLKGNCSEDLFCILKSTPSKSWA-YLQVSKHLNNTK 117
| : ||| : : : | ||| : : : | : : : | : : : | : : : | : : : |
| : ||| : : : | ||| : : : | : : : | : : : | : : : | : : : |

Db 344 IYVSEGDGKAAVY-TRAILARSPPWFIV-DRPFLP-CTRHN 383
QY 118 LSNWEDGTIHLVQGNLIVQFPGLYFIVQLQFLVQCSNHS 160
| : ||| : : : | : : : | : : : | : : : | : : : | : : : |
| : ||| : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 8
ID VD10_SFVKA STANDARD; PRT; 260 AA.
AC P32097;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DE PROTEIN D10.
DE D10P.
GN SHOR.
OS SHOR FIBROMA VIRUS (STRAIN KASZA) (SFV).
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; POXVIRIDAE; CHORDOPOXVIRINAE;
OC LEPORIPXVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92074222.
RA STRAYER D.S., JERNG H.H., O'CONNOR K.;
RT "Sequence and analysis of a portion of the genomes of Shope fibroma
virus and malignant rabbit fibroma virus that is important for viral
replication in lymphocytes.";
RL VIROLOGY 185:585-595(1991).
CC -1- SIMILARITY: TO PROTEINS WITH A CORE MUTT DOMAIN.
CC -----
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CC -----
DR EMBL; M74532; -; NOT_ANNOTATED_CDS.
DR PROSITE; PS00893; MUTT; 1.
DR PFAM; PF00293; mutt; 1.
FT DOMAIN 124 157 MUTT-LIKE.
SQ SEQUENCE 260 AA; 30460 MW; C35DDF27 CRC32;

Query Match 6.1%; Score 104; DB 1; Length 260;
Best Local Similarity 30.2%; Pred. No. 2.63e-02;
Matches 16; Conservative 19; Mismatches 15; Indels 3; Gaps 3;

Db 147 EINDSDIYD-SRPFVH-LFIEDLLSNRVYETILFLGNTLTLSNEILNNFL 197
QY 183 ESGVQSKNIYQNLSQLHLYLQVNSTISRV-DNFQYVDTNTFPDLNVLVSL 234
| : ||| : : : | : : : | : : : | : : : | : : : | : : : |
| : ||| : : : | : : : | : : : | : : : | : : : | : : : |

RESULT 9
ID FASL_RAT STANDARD; PRT; 278 AA.
AC P36940;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE FAS ANTIGEN LIGAND.
GN APTLGI OR FASL.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94084792.
RA SUDA T., TAKAHASHI T., GOLSTEIN P., NAGATA S.;
RT "Molecular cloning and expression of the Fas ligand, a novel member
of the tumor necrosis factor family.";
RL CELL 75:1169-1178(1993).
CC -1- FUNCTION: CITOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
T CELLS, OR BOTH.
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
SURFACE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
KIDNEY AND LUNG.
CC -1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U03470; G440179; .
DR PROSITE; PS00251; TNF_1; 1.
DR PFAM; PF00229; TNF; 1.
```

KW CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR; APOPTOSIS.
 FT DOMAIN 1 77 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 78 99 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 100 278 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 4 69 PRO-RICH.
 FT DOMAIN 45 58 POLY-PRO.
 FT DISULFID 199 230 BY SIMILARITY.
 FT CARBOHYD 116 116 POTENTIAL.
 FT CARBOHYD 247 247 POTENTIAL.
 FT CARBOHYD 257 257 POTENTIAL.
 FT CARBOHYD 116 116 POTENTIAL.
 FT CARBOHYD 247 247 POTENTIAL.
 FT CARBOHYD 257 257 POTENTIAL.
 SQ SEQUENCE 278 AA; 31140 MW; 6DC17725 CRC32;

Query Match 5.9%; Score 101; DB 1; Length 278;
 Best Local Similarity 33.3%; Pred. No. 7.33e-02;
 Matches 16; Conservative 13; Mismatches 15; Indels 4; Gaps 3;

Db 157 LEWEDYGTALISGVKYGGLVINEAGLVFVYKVFGRQSCNSOPL 204
 QY 118 LSWNEG-GR--IHGLYQDGNLIVQFGLFVIVCQLQFLVQ-CSNSHV 161

RESULT 10
 ID FUCR_HAEIN STANDARD; PRT; 249 AA.
 AC P44780.
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE L-FUCOSE OPERON ACTIVATOR.
 GN FUCR OR HI0615.
 OS HAEMOPHILUS INFLUENZAE.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
 OC HAEMOPHILUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20;
 RX MEDLINE; 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLVACHE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCCANNEN K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRITCHMAN J.L., FUHRMAN J.L., GEOGHAGEN N.S.M.,
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 influenzae Rd.";
 RL SCIENCE 269:496-512(1995).
 CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE FUC OPERON
 CC (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC -----
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 CC -----
 CC EMBL; U32744; G1573609; -
 DR TIGR; HI0615; -
 DR PROSITE; PS00894; HTH_DEOR_FAMILY; 1.
 DR PFAM; PF00455; GEOR; 1.
 KW FUCOSE METABOLISM; TRANSCRIPTION REGULATION; ACTIVATOR;
 FT DNA-BINDING.
 FT DNA_BIND 18 37 H-T-H MOTIF (POTENTIAL).
 SQ SEQUENCE 249 AA; 28163 MW; 9ECE74A2 CRC32;

Query Match 5.8%; Score 99; DB 1; Length 249;
 Best Local Similarity 19.6%; Pred. No. 1.43e-01;
 Matches 21; Conservative 35; Mismatches 46; Indels 5; Gaps 5;

Db 64 SFFQTRKHINATA-KRHIAOKALDLYENAVIGLDASSTWSYFAYLMP-DIPCTVVTNSM 121
 QY 105 AYLOVSKHLNNTKLSWNEGTGHIYQDGNLIVQFGL-FYIVCQLQFLVQCSNHSVDL 163

Db 122 FNINALVN-KSNVKTIVTGGVYSAKYEAFFGLSEYLLQRLHNFVS 167
 QY 164 -TLQLLSKIRKQTLTVCSGVSQSKNIYQNSQFLHLYLQVNSTI 209

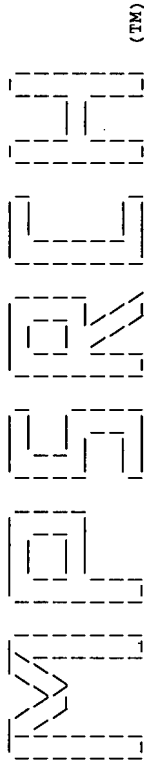
RESULT 11
 ID TH17 YEAST STANDARD; PRT; 598 AA.
 AC Q05998; P87335;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE THIAMINE TRANSPORTER.
 GN TH17 OR TH110 OR YLR237W OR L8083.2.
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCCHAROMYCETALES;
 OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GRF88;
 RA ENJO F.;
 RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
 RA FAVELLO A., FULTON L., GAITUNG S., GRECO T., KIRSTEN J., KUCABA T.,
 RA HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
 RA JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,
 RA MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
 RA TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOLDMAN P., VAUDIN M.,
 RA WILSON R., WATERSTON R.;
 RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- FUNCTION: RESPONSIBLE FOR INTAKE OF THIAMINE.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE ALLANTOIN PERMEASE FAMILY. STRONG, TO
 CC YOR071C AND YOR192C.
 CC -----
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 CC -----
 CC EMBL; U19027; G609365; -
 DR EMBL; D55634; G1871134; -
 DR SGD; L0003514; TH17
 KW TRANSMEMBRANE; TRANSPORT.
 FT TRANSMEM 42 62 POTENTIAL.
 FT TRANSMEM 74 94 POTENTIAL.
 FT TRANSMEM 112 132 POTENTIAL.
 FT TRANSMEM 174 194 POTENTIAL.
 FT TRANSMEM 178 218 POTENTIAL.
 FT TRANSMEM 241 261 POTENTIAL.
 FT TRANSMEM 275 295 POTENTIAL.
 FT TRANSMEM 333 353 POTENTIAL.
 FT TRANSMEM 372 392 POTENTIAL.
 FT TRANSMEM 395 415 POTENTIAL.
 FT TRANSMEM 447 467 POTENTIAL.
 FT TRANSMEM 484 504 POTENTIAL.
 SQ SEQUENCE 598 AA; 66904 MW; 79F16ACD CRC32;

Query Match 5.8%; Score 100; DB 1; Length 598;
 Best Local Similarity 30.2%; Pred. No. 1.03e-01;

[illegible]

QY 174 KKOTLVTV 181

Search completed: Fri Aug 13 16:37:23 1999
Job time : 16 secs.



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MPPerch_pp    protein - protein database search, using Smith-Waterman algorithm
Run on:       Fri Aug 13 16:37:41 1999;    MasPar time 16.69 Seconds
              781.448 Million cell updates/sec
Tabular output not generated.

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>US-09-079-785-6
Title:
Description: (1-239) from US09079785.pap
Perfect Score: 1719
Sequence: 1 MPEGLQAGSCGAPSPDPM.....DTNTEPLDNVLSVFLYSSD 239
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Scoring table: PAM 150
Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Database:
sptrembl9
1:sp__archaea 2:sp__bacteria 3:sp__fungi 4:sp__human
5:sp__invertebrate 6:sp__mammal 7:sp__mhc 8:sp__organelle
9:sp__phage 10:sp__plant 11:sp__rodent 12:sp__unclassified
13:sp__vertebrate 14:sp__virus

Statistics:
Mean 44.769; Variance 84.018; scale 0.533
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description	Pred. No.
	Score	Match	Length				
1	1199	69.7	234	4	Q43404	CD30L PROTEIN.	5.08e-231
2	114	6.6	279	11	O61217	FAS LIGAND.	4.13e-03
3	111	6.5	479	11	Q64538	PHOSPHOPROTEIN PHOSPHA	1.13e-02
4	111	6.5	499	11	Q35299	PROTEIN PHOSPHATASE 5.	1.13e-02
5	104	6.1	619	3	Q99324	CHROMOSOME XV READING	1.11e-01
6	103	6.0	693	6	Q27960	SODIUM-DEPENDENT PHOSP	1.53e-01
7	103	6.0	2051	5	O44328	RECEPTOR TYROSINE PHOS	1.53e-01
8	100	5.8	249	4	O43508	TWEAK.	3.92e-01
9	100	5.8	332	10	Q22985	RIBITOL DEHYDROGENASE	3.92e-01
10	100	5.8	492	13	Q42205	PROTEIN PHOSPHATASE 5	3.92e-01
11	100	5.8	1010	5	Q20818	F55C5.4 PROTEIN.	3.92e-01
12	96	5.6	414	5	P91486	SIMILARITY TO QUAIL NE	1.34e+00
13	96	5.6	1111	2	O85522	HYPERLACTIC 119.9 KD	1.34e+00
14	96	5.6	1198	2	Q53730	POLYKETIDE SYNTHASE (F	1.34e+00
15	96	5.6	4910	3	Q12019	SIMILARITY NEAR N-TERM	1.34e+00
16	94	5.5	184	2	O31333	EC541A PROTEIN (FRAGME	2.44e+00
17	94	5.5	203	5	O15934	TB65.3 PROTEIN.	2.44e+00
18	95	5.5	419	5	O77212	CYCLIN A.	1.81e+00
19	94	5.5	434	10	O64886	PUTATIVE HEME A:FARNES	2.44e+00
20	95	5.5	445	10	O39077	HOMOLOG OF DTPD-GLUCOS	1.81e+00

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RESULT 2
ID Q61217 PRELIMINARY; PRT; 279 AA.
AC Q61217;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FAS LIGAND.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RA FENNER M.H., SHIODA T., ISSELBACHER K.J.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U58995; G1389772; -
DR PROSITE; PS00251; TNE_1; 1.
DR PFAM; PF00229; TNE; 1.
SQ SEQUENCE 279 AA; 31340 MW; 9062DF08 CRC32;

Query Match 6.5%; Score 114; DB 11; Length 279;
Best Local Similarity 32.3%; Pred. No. 4.13e-03;
Matches 20; Conservative 15; Mismatches 23; Indels 4; Gaps 3;

Db 145 AHLTGNPHSRISPLEWEDTYGTALISGVKKGLVINEAGLYFVYSKYVFGSGNNQP 204
QY 105 AYLVQSKHLNLTLSWNEED-GT--IHGLIYQDGNLIVFPFGLFYVCOQLVQ-CSNHS 160
Db 205 LN 206
QY 161 VD 162

RESULT 3
ID Q64538 PRELIMINARY; PRT; 479 AA.
AC Q64538;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PHOSPHOPROTEIN PHOSPHATASE (FRAGMENT).
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LUNG;
RX MEDLINE; 95062208.
RA CHINKERS M.;
RT "Targeting of a distinctive protein-serine phosphatase to the protein
RT kinase-like domain of the atrial natriuretic peptide receptor.";
RL PROC. NATL. ACAD. SCI. U.S.A. 91:11075-11079(1994).
DR EMBL; U12203; G1663530; -
DR PFAM; PF00149; Stposphatase; 1.
DR PFAM; PF00515; TPR; 2.
FT NON_TER 1
SQ SEQUENCE 479 AA; 54718 MW; 0F812560 CRC32;

Query Match 6.5%; Score 111; DB 11; Length 479;
Best Local Similarity 25.8%; Pred. No. 1.13e-02;
Matches 23; Conservative 28; Mismatches 30; Indels 8; Gaps 8;

Db 188 CAYQILVQ-VKE-V-LCKLSTLVETLTKETKIVC-GDTHGQ-FYDLLNIFELNGLPSE 242
QY 148 COLQFLVQCSNHSVDL-TLQLLINSKIKKQTLTVTCESGVQSKNIYQNLSQLFLHLYQVN 206
Db 243 TNPYI-FNG-DFVDRGSFSVEVILTLFGF 269
QY 207 STISVRVDNFQYVDNTFTPLDNVLSVELY 235

RESULT 4
ID Q35299 PRELIMINARY; PRT; 499 AA.
AC Q35299;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PROTEIN PHOSPHATASE 5.
GN PP5.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA OLLENDORFF V., DONOGHUE D.J.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF018262; G2407637; -
DR PFAM; PF00149; Stposphatase; 1.
DR PFAM; PF00515; TPR; 2.
SQ SEQUENCE 499 AA; 56846 MW; 46E531D4 CRC32;

Query Match 6.5%; Score 111; DB 11; Length 499;
Best Local Similarity 25.8%; Pred. No. 1.13e-02;
Matches 23; Conservative 28; Mismatches 30; Indels 8; Gaps 8;

Db 208 CAYQILVQ-VKE-V-LCKLSTLVETLTKETKIVC-GDTHGQ-FYDLLNIFELNGLPSE 262
QY 148 COLQFLVQCSNHSVDL-TLQLLINSKIKKQTLTVTCESGVQSKNIYQNLSQLFLHLYQVN 206
Db 263 TNPYI-FNG-DFVDRGSFSVEVILTLFGF 289
QY 207 STISVRVDNFQYVDNTFTPLDNVLSVELY 235
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RESULT 5
ID Q99234 PRELIMINARY; PRT; 619 AA.
AC Q99234;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CHROMOSOME XV READING FRAME ORF YOR030W.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
OC SACCHAROMYCETACEAE; SACCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RA DE HAAN M., GRIVELL L.A., MAARSE A.C.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RA DE HAAN M., MAARSE A.C., GRIVELL L.A.;
RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE; 94019318.
RA DUMONT M.E., SCHLICHTER J.B., CARDILLO T.S., HAYES M.K., BETHLENDY G.;
RA SHERMAN F.;
RT "CYC2 encodes a factor involved in mitochondrial import of yeast
RT cytochrome c.";
RL MOL. CELL. BIOL. 13:6442-6451(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679.
RX MEDLINE; 94169519.
RA LEE Y.S., SHIMIZU J., YODA K., YAMASAKI M.;
RT "Molecular cloning of a gene, DHS1, which complements a
RT drug-hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
RL BIOSCI. BIOTECHNOL. BIOCHEM. 58:391-395(1994).
DR EMBL; 274938; E252327; -
DR EMBL; X87331; G829140; -
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AC O42205;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PROTEIN PHOSPHATASE 5 (FRAGMENT).
GN PP5.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBRACHIA; PIPIDAE; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RA OLLENDORFF V., DONOGHUE D.J.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF018263; G2407639; -
DR PFAM; PF00149; Stposphatase; 1.
DR PFAM; PF00515; TPR; 2.
FT NON_TER 1
SQ SEQUENCE 492 AA; 56144 MW; C503341E CRC32;

Query Match 5.8%; Score 100; DB 13; Length 492;
Best Local Similarity 22.7%; Pred. No. 3.92e-01;
Matches 20; Conservative 28; Mismatches 34; Indels 6; Gaps 6;

Db 201 CLYQMLVQVXD-ILS-KLPISLVEVLEKSOQVTC-GDTHGQ-FYDLNMFHNLGSPEN 256
QY 148 CQQLVQCSNHSVDLTQLLLINSKIKQTLTVCSGVSKNIYQNSQLFLHYLVNS 207

Db 257 NPVI-FNG-DFVDRGFSVEIVTLFG 282
QY 208 TISVRVDFNQYVDTNFPFLDNVLSVFLY 235

RESULT 11
ID Q20818 PRELIMINARY; PRT; 1010 AA.
AC Q20818;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE F55CS.4 PROTEIN.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEAE; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RA HARRIS B.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL NATURE 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC STRAIN-BRISTOL N2;
RA DU Z., MAGGI L.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U80440; G1703600; -.
SQ SEQUENCE 414 AA; 46525 MW; EB685192 CRC32;

Query Match 5.6%; Score 96; DB 5; Length 414;
Best Local Similarity 31.5%; Pred. No. 1.34e+00;
Matches 17; Conservative 15; Mismatches 19; Indels 3; Gaps 3;

Db 322 PGIEVKNYIP-LPQHLLKKRSPISVHNKIEKNLATTTTTTFLHMLLFLY 374
QY 184 SGVQS-KNIYQNSQLFLHYLVN-STISVRVDFNQYVDTNFPFLDNVLSVFLY 235

RESULT 13
ID O86522 PRELIMINARY; PRT; 1111 AA.
AC O86522;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 119.9 KD PROTEIN.
GN SC1C2.21C.
OS STREPTOMYCES COELICOLOR.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; STREPTOMICINAE; STREPTOMICETACEAE; STREPTOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-A3(2);
RA MURPHY L., HARRIS D.;
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
```

```
Db 297 ACLTAFETYG 305
QY 228 NVLSVFLY 236

RESULT 12
ID P91486 PRELIMINARY; PRT; 414 AA.
AC P91486;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SIMILARITY TO QUAIL NEURONAL CELL CYCLE WITHDRAWAL PROTEIN.
GN T21E12.2
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEAE; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL NATURE 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC STRAIN-BRISTOL N2;
RA DU Z., MAGGI L.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U80440; G1703600; -.
SQ SEQUENCE 414 AA; 46525 MW; EB685192 CRC32;

Query Match 5.6%; Score 96; DB 5; Length 414;
Best Local Similarity 31.5%; Pred. No. 1.34e+00;
Matches 17; Conservative 15; Mismatches 19; Indels 3; Gaps 3;

Db 322 PGIEVKNYIP-LPQHLLKKRSPISVHNKIEKNLATTTTTTFLHMLLFLY 374
QY 184 SGVQS-KNIYQNSQLFLHYLVN-STISVRVDFNQYVDTNFPFLDNVLSVFLY 235

RESULT 13
ID O86522 PRELIMINARY; PRT; 1111 AA.
AC O86522;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 119.9 KD PROTEIN.
GN SC1C2.21C.
OS STREPTOMYCES COELICOLOR.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; STREPTOMICINAE; STREPTOMICETACEAE; STREPTOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-A3(2);
RA MURPHY L., HARRIS D.;
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
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OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 GN L8004.13.
 GN
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;

W P S R L

(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:40:49 1999; MasPar time 10.77 Seconds
Tabular output not generated. 461.930 Million cell updates/sec

Title: >US-09-079-785-8
Description: (1-234) from US09079785.pep
Perfect Score: 1697
Sequence: 1 MDPGLQQALNGMAPPDFTAM.....DTSTFPLENVLISFLYSNSD 234

Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 32.612; Variance 156.592; scale 0.208

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1697	100.0	234	8 R45009	Sequence encoded by a	6.59e-137
2	1566	92.3	215	8 R45007	Sequence encoded by a	2.93e-125
3	1232	72.6	239	8 R45008	Sequence encoded by a	1.19e-95
4	1189	70.1	220	8 R45006	Sequence encoded by a	7.50e-92
5	118	7.0	154	3 F50502	Human tumour necrosis	1.08e+00
6	118	7.0	180	23 W10875	FasL/TL-alpha hybrid.	1.08e+00
7	115	6.8	137	14 R79067	Mouse Fas ligand (par	1.75e+00
8	115	6.8	138	14 R79068	Mouse Fas ligand (par	1.75e+00
9	115	6.8	157	23 W10877	TNFR/TL-alpha hybrid.	1.75e+00
10	115	6.8	157	12 R62470	Tumour necrosis facto	1.75e+00
11	115	6.8	179	14 R79069	Mouse Fas ligand (par	1.75e+00
12	115	6.8	279	18 R88357	Mouse Fas ligand.	1.75e+00
13	115	6.8	279	18 R77282	Mouse Fas-L protein.	1.75e+00
14	115	6.8	279	14 R79098	Mouse Fas ligand.	1.75e+00
15	113	6.7	151	1 P81323	Anti-tumour peptide.	2.41e+00
16	114	6.7	216	38 W68412	Hybrid alpha-1-thymos	2.06e+00

17	112	6.6	154	11 R59578	Human TNF mutein.	2.83e+00
18	111	6.5	130	14 R79096	Human Fas ligand C-te	3.32e+00
19	111	6.5	136	33 W48955	Fas ligand fragment (3.32e+00
20	111	6.5	136	14 R88307	N-terminally deleted	3.32e+00
21	111	6.5	137	14 R79100	Human Fas ligand (par	3.32e+00
22	111	6.5	137	14 R88306	N-terminally deleted	3.32e+00
23	111	6.5	138	14 R88305	N-terminally deleted	3.32e+00
24	111	6.5	138	14 R79064	Human Fas ligand (par	3.32e+00
25	111	6.5	139	14 R88304	N-terminally deleted	3.32e+00
26	111	6.5	141	14 R88303	N-terminally deleted	3.32e+00
27	111	6.5	145	27 W35848	Human Fas-Ligand for	3.32e+00
28	110	6.5	150	1 P81066	Sequence of new physi	3.89e+00
29	111	6.5	151	26 W16667	Human Fas ligand (hfa	3.32e+00
30	111	6.5	158	4 R22723	TNF polypeptide mutei	3.32e+00
31	110	6.5	161	4 R22308	TNF polypeptide mutei	3.89e+00
32	111	6.5	178	14 R88308	C-terminally deleted	3.32e+00
33	111	6.5	179	14 R79099	Human Fas ligand (par	3.32e+00
34	111	6.5	179	23 W1814	Fas ligand.	3.32e+00
35	111	6.5	265	33 W48954	Non-cleavable Fas lig	3.32e+00
36	111	6.5	268	33 W48953	Non-cleavable Fas lig	3.32e+00
37	111	6.5	281	14 R77281	Human Fas-L protein.	3.32e+00
38	111	6.5	281	36 W75959	Human Fas ligand.	3.32e+00
39	111	6.5	281	14 R79097	Human Fas ligand.	3.32e+00
40	111	6.5	281	18 R88356	Fas Ligand.	3.32e+00
41	111	6.5	281	35 W49105	Human Fas ligand deri	3.32e+00
42	111	6.5	281	18 R98104	Human Fas ligand.	3.32e+00
43	111	6.5	281	26 W27143	Human Fas ligand.	3.32e+00
44	111	6.5	287	26 W27146	CH3/Fas ligand domain	3.32e+00
45	111	6.5	378	27 W35864	Human Fas-Ligand:igG2	3.32e+00

ALIGNMENTS

RESULT 1
ID R45009 standard; Protein; 234 AA.

AC R45009;
DT 19-JUN-1994 (first entry)
DE Sequence encoded by a human CD30-L cDNA clone
DE Encoding additional N-terminal amino acids.
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF;
OS Homo sapiens.
FH Key Location/Qualifiers
FT region 41..62 /label= Transmembrane
FT WO9324135-A.
PN 09-DEC-1993.
PD 25-MAY-1993; U04926.
PF 26-MAY-1992; US-889717.
PR 02-JUN-1992; US-892459.
PR 15-JUN-1992; US-899660.
PR 01-JUL-1992; US-907224.
PR 27-OCT-1992; US-966775.
PA (IMV) IMMUNEX CORP.
PI Amritage RJ Goodwin RG, Smith CA;
DR WPI; 93-405417/50.
DR N-PSDB; Q53538.
PT New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
PS Claim 15: Figure 7a: 59pp: English.
CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prepd. from
CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC (Q53535). This cDNA can then be used as a probe to screen a human PBL
CC cDNA library to obtain cDNA encoding human CD30-L (Q53536). An anchored
CC PCR technique was employed to isolate CD30-L human and murine clones
CC containing an additional 19 N-terminal amino acid sequence (Q53537,

```
CC Q53538).
SQ Sequence 234 AA;
  Query Match 100.0%; Score 1697; DB 8; Length 234;
  Best Local Similarity 100.0%; Pred. No. 6.59e-137; Mismatches 0; Indels 0; Gaps 0;
  Matches 234; Conservative 0;

Db 1 mdpglqalngmappgdgtamhvpagvashlgttsrsyfyllttatlaclclvftatimvl 60
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 MDPLGQALNGMAPPDGTAMHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTATIMVL 60

Db 61 vvgtrdsipndvplkgncsedllclilkrappfkkswaylqvahlnktlswkndgl 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VVGTRDSIPNDVPLKGCNSEDLLCLILKRAPPFKKSWAYLQVAKHLNKTLSWNKNDGI 120

Db 121 lhgvyqdnvlgfpglyfiicqlqflvcpcnnsvdllklllnkhkqalvtvcesg 180
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LHGVRVQDGNLVIOFPGLYFIICQLQFLVCPNNSVDLLKLLINKHKKQALVTVCESG 180

Db 181 mtkkhvqnlsgfllldylgvnttisivndtfgvidtstfplenvlsiflynsd 234
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 MTKKHVQNLSGFLLDYLGVNTTISVNDTFQYIDSTFTPLENLSIFLYNSD 234

RESULT 2
ID R45007 standard; Protein: 215 AA.
AC R45007;
DT 19-JUN-1994 (first entry)
DE Sequence encoded by a human CD30-L cDNA clone.
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
OS Homo sapiens.
FH Key Location/Qualifiers
FT region 22..43
FT /label= transmembrane
PN WO9324135-A.
PD 09-DEC-1993.
PF 25-MAY-1993; U04926.
PR 26-MAY-1992; US-889717.
PR 02-JUN-1992; US-892459.
PR 15-JUN-1992; US-899660.
PR 01-JUL-1992; US-907224.
PR 27-OCT-1992; US-966775.
PA (IMV ) IMMUNEX CORP.
PI Armitage RJ, Goodwin RG, Smith CA;
DR WPI: 93-405417/50.
DR N-PSDB: Q53536.
PT New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
PS Claim 15; Figure 5a; 59pp; English.
CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prepd. from
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC (Q53535). This cDNA can then be used as a probe to screen a human PBL
CC cDNA library to obtain cDNA encoding human CD30-L (Q53536). An anchored
CC PCR technique was employed to isolate CD30-L human and murine clones
CC containing an additional 19 N-terminal amino acid sequence (Q53537,
CC Q53538).
SQ Sequence 239 AA;
  Query Match 72.6%; Score 1232; DB 8; Length 239;
  Best Local Similarity 70.0%; Pred. No. 1.19e-95;
  Matches 168; Conservative 39; Mismatches 26; Indels 7; Gaps 3;

Db 1 mepglqagscapspdpamvqpgsvasprstwrstsrstsfylsttal-vclvvav 59
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 MDPLGQALNGMAPPDGTAMHVPAGSVASHL-GT-----TSRSYFYLTTATLALCLVFTV 54

Db 60 aillvlvqkdstpttkekaplkgncsedlftlktstpskkswaylqvskhlnntkls 119
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 55 ATIMVLVQRTSIPNSPDNVPFLKGCNSEDLLCLILKRAPPFKKSWAYLQVAKHLNKTLS 114

Db 120 wnedgtihelivqdnlgvfpglyfiicqlqflvcpcnnsvdllklllnkhkqalvt 179
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 WNKGDLHGVRVQDGNLVIOFPGLYFIICQLQFLVCPNNSVDLLKLLINKHKKQALV 174

Db 180 tvcesgqskniyqnlsgfllldylgvnttisivndtfgvidtstfplenvlsiflynsd 239
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 TVCESGMQTKHVVQNLSGFLLDYLGVNTTISVNDTFQYIDSTFTPLENLSIFLYNSD 234
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RESULT 4
ID R45006 standard; Protein; 220 AA.
AC R45006;
DE 19-JUN-1994 (first entry)
DE Sequence encoded by a murine CD30-L cDNA clone.
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
OS Acromys caliginus.
FH Key Location/Qualifiers
FT region 28..48
FT /label= transmembrane
FT
FT WO9324135-A.
PD 09-DEC-1993.
PF 25-MAY-1993; U04926.
PR 26-MAY-1992; US-889717..
PR 02-JUN-1992; US-892459..
PR 15-JUN-1992; US-899660.
PR 01-JUL-1992; US-907224.
PR 27-OCT-1992; US-966775.
PA (IMMV) IMMUNEX CORP.
PI Armitage RJ, Goodwin RG, Smith CA;
WPI: 93-405417/50.
DR N-PSDB; Q53535.
PT New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
PS Claim 15; Figure 3a; 59pp; English.
CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prepd. from
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
CC This cDNA can then be used as a probe to screen a human PBL cDNA
CC library to obtain cDNA encoding human CD30-L.
CC Sequence 220 AA;
Query Match 70.1%; Score 1189; DB 8; Length 220;
Best Local Similarity 73.8%; Pred. No. 7.50e-92;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;
Db 20 stersylsttal-vcvlvavailvvlvqkdstnttekapkngncsedlfcitks 78
QY 33 TTSRSYFLTTATLALCLVFTVATIMVLVQRTDSIPNSPDVPLKGNCSDELICILKR 92
Db 79 tpekkswaylqvskhlntklswnedgtihglydgnllvqfpglyfvcqlglvqcs 138
QY 93 APFKKSWAYLQVAKHLNKLKLSWNGDKILHGVRVQDGNLVIQFPLFIICQLQF 152
Db 139 nhsvdltclgllnskikktlvtvcsgvskniyqlsqfllhylvgnstisvrvdnfq 198
QY 153 NNSVDLLELLLNKHKKQALVTVCSGMQTKVYQNLQSLDYLQVNTTISVNVDTQF 212
Db 199 yvdtntfpldnvlsflysssd 220
QY 213 YIDTSIFPLENLSIFLYNSD 234
RESULT 5
ID P50502 standard; Protein; 154 AA.
AC P50502;
DE 22-OCT-1991 (first entry)
DE Human tumour necrosis factor.
KW Tumour necrosis factor; antitumour agent; antiviral agent; plasmid pRGE;
KW plasmid pRGE.
OS Homo sapiens.
PN BE-902119-A.
PD 04-OCT-1985.
PF 06-APR-1984; 597372.
PR 06-APR-1984; US-597372.
PA (ASAH) Asahi Kasei Kogyo.
DR WPI: 85-256098/42.
DR N-PSDB; N50479.
FT New human tumour necrosis factor polypeptide - useful as antitumour
FT and antiviral agent, and DNA sequences coding for it.
PS Claim 1; page 68; 84pp; french.
CC DNA encoding the human tumour necrosis factor is extracted from,
CC eg pancreatic tissue. The DNA is expressed in plasmids pRGE or pRGE
CC using E.coli K12 JM83(pRGE) or JM83(pHGE), deposited as ATCC 39655 and
CC 39656, resp. The human tumour necrosis factor is used as an antitumour
CC and antiviral agent, pref. administered parenterally.
CC Sequence 154 AA;
Query Match 7.0%; Score 118; DB 3; Length 154;
Best Local Similarity 37.5%; Pred. No. 1.08e-00;
Matches 27; Conservative 13; Mismatches 26; Indels 6; Gaps 5;
Db 3 rtpmdkpvahl-vanpqaeqglqlwnrranallangvelrdqvlvpsdglylysqvlf 61
QY 92 RAPFKKSWAYLQVAKHLNKLKLSW-NK--DGIL-HGVRYQDGNLVIQFPLFIICQLQF 147
Db 62 kgqgcpssthvll 73
QY 148 LVQ-CPNNSVDL 158
RESULT 6
ID WI0875 standard; Protein; 180 AA.
AC WI0875;
DE 25-SEP-1997 (first entry)
DE FasL/TN-alpha hybrid.
KW C-terminal extracellular domain; CD40 ligand; mutated; trimerisation;
KW lymphotoxin; LT; beta; alpha; tumour necrosis factor; TNF; inhibitor;
KW signalling; receptor; Fas; treating; autoimmune disease; diabetes;
KW rheumatoid arthritis; inflammatory bowel disease; HIV proliferation;
KW immune response; tissue graft.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_difference 44
FT /note= "LT-alpha subunit association domain residue"
FT misc_difference 68..70
FT /note= "LT-alpha subunit association domain residues"
FT misc_difference 70
FT /note= "given as 0 in the specification"
FT misc_difference 92
FT /note= "LT-alpha subunit association domain residue"
FT misc_difference 94
FT /note= "LT-alpha subunit association domain residue"
FT misc_difference 122..127
FT /note= "LT-alpha subunit association domain residues"
FT misc_difference 126
FT /note= "given as 0 in the specification"
FT misc_difference 129..130
FT /note= "LT-alpha subunit association domain residues"
FT misc_difference 139
FT /note= "LT-alpha subunit association domain residue"
FT misc_difference 146
FT /note= "LT-alpha subunit association domain residue"
FT misc_difference 172
FT /note= "LT-alpha subunit association domain residue"
FT misc_difference 177..178
FT /note= "LT-alpha subunit association domain residues"
FT WO9640774-A1.
PD 19-DEC-1996.
PF 06-JUN-1996; U09773.
PR 07-JUN-1995; US-476074.
PA (BIOJ) BIOGEN INC.
PI Browning JL, Karpusas MN, Meier W;
DR WPI: 97-087055/08.
PT Heteromeric complexes comprising lymphotoxin sub-units - useful as
PT inhibitors of signalling by TNF- and TNF-related receptors, for
PT treating auto-immune disease, graft rejection, etc.

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PS Disclosure: Fig 10; 87pp; English.
 CC This sequence comprises the C-terminal extracellular domain of the Fas
 CC ligand altered to drive trimerisation with wild-type lymphotoxin (LT)-
 CC beta. LT subunit association domains potentiate subunit associations into
 CC an active trimeric ligand. Tumour necrosis factor (TNF)-related ligand
 CC monomers mutated in their respective subunit associations domains can
 CC form heteromeric complexes with LT subunits. LT-alpha/beta heteromeric
 CC complexes and LT heterotrimeric complexes are useful as inhibitors of
 CC signalling by TNF receptors (R) and TNF-related receptors, such as CD40,
 CC FAS and LT-beta receptors. By inhibiting TNF-R signalling the complexes
 CC (esp., LT-alpha2/beta1) can be used for treating autoimmune diseases
 CC including diabetes, rheumatoid arthritis, inflammatory bowel disease and
 CC HIV proliferation, known to be improved by TNF inhibition. The complexes
 CC are also useful for preventing or reducing the severity of an immune
 CC response to a tissue graft.
 CC Sequence 180 AA;

Query Match 7.0%; Score 118; DB 23; Length 180;
 Best Local Similarity 31.4%; Pred. No. 1.08e+00;
 Matches 27; Conservative 19; Mismatches 33; Indels 7; Gaps 6;

Db 41 lrlka-ahl-tgksnrsmplewedytgiwlgxvkkkgglvinetglyfvyxvfrqg 98
 QY 95 FKSWAYLOVAKHLNKT-KLSWVKD-GI--LHGVRQDGNLVIFPGLYFIICQLQFLVQ 150
 Db 99 scnnlpishkvymrnsqypqdlvlls 124
 QY 151 -CPNNSVDLKLLELLINKHKKQALVT 175

RESULT 7
 ID R79067 standard; Protein: 137 AA.
 AC R79067;
 DT 22-FEB-1996 (first entry)
 DE Mouse Fas ligand (partial sequence).
 KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
 KW Fas cell surface antigen; Fas-L; mouse.
 OS Mus musculus.
 PN W09513293-AL.
 PD 18-MAY-1995.
 PF 10-NOV-1994; J01899.
 PR 10-NOV-1993; JP-305975.
 PR 13-DEC-1993; JP-342526.
 PR 18-MAR-1994; JP-074344.
 PR 08-JUL-1994; JP-180955.
 PR 07-SEP-1994; JP-239363.
 PR 18-OCT-1994; JP-278378.
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PA (OSAB-) OSAKA BIOSCIENCE INST.
 PI Nagata S, Nakamura N, Suda T, Takahashi T;
 DR WPI: 95-194031/25.
 DR N-PSDB; Q99496.
 PT Peptide which binds to Fas antigen, and antibody reactive with it -
 PT for treatment and diagnosis of viral or auto:immune diseases
 PS Claim 9; Page 219-221; 300pp; Japanese.
 CC Fas ligands or active fragments able to induce apoptosis in cells
 CC which express the Fas cell surface antigen are claimed. The present
 CC proteins are isolated from human, rat and mouse sources. The present
 CC sequence represents part of the mouse Fas ligand.
 SQ Sequence 137 AA;

Query Match 6.8%; Score 115; DB 14; Length 137;
 Best Local Similarity 35.4%; Pred. No. 1.75e+00;
 Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 3 ahltnphrsrslplewedytgallsgvkkkgglvinetglyfvyxvfrqgcnngp 62
 QY 100 AYLOVAKHLNKTLSWVKD-GI-L-HGVRQDGNLVIFPGLYFIICQLQFLVQ-CPNNS 155
 Db 63 lnhkv 67
 QY 156 VDLKL 160

RESULT 8
 ID R79068 standard; Protein: 138 AA.
 AC R79068;
 DT 22-FEB-1996 (first entry)
 DE Mouse Fas ligand (partial sequence).
 KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
 KW Fas cell surface antigen; Fas-L; mouse.
 OS Mus musculus.
 PN W09513293-AL.
 PD 18-MAY-1995.
 PF 10-NOV-1994; J01899.
 PR 10-NOV-1993; JP-305975.
 PR 13-DEC-1993; JP-342526.
 PR 18-MAR-1994; JP-074344.
 PR 08-JUL-1994; JP-180955.
 PR 07-SEP-1994; JP-239363.
 PR 18-OCT-1994; JP-278378.
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PA (OSAB-) OSAKA BIOSCIENCE INST.
 PI Nagata S, Nakamura N, Suda T, Takahashi T;
 DR WPI: 95-194031/25.
 DR N-PSDB; Q99497.
 PT Peptide which binds to Fas antigen, and antibody reactive with it -
 PT for treatment and diagnosis of viral or auto:immune diseases
 PS Claim 10; Page 221-222; 300pp; Japanese.
 CC Fas ligands or active fragments able to induce apoptosis in cells
 CC which express the Fas cell surface antigen are claimed. The present
 CC proteins are isolated from human, rat and mouse sources. The present
 CC sequence represents part of the mouse Fas ligand.
 SQ Sequence 138 AA;

Query Match 6.8%; Score 115; DB 14; Length 138;
 Best Local Similarity 35.4%; Pred. No. 1.75e+00;
 Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;
 Db 4 ahltnphrsrslplewedytgallsgvkkkgglvinetglyfvyxvfrqgcnngp 63
 QY 100 AYLOVAKHLNKTLSWVKD-GI-L-HGVRQDGNLVIFPGLYFIICQLQFLVQ-CPNNS 155
 Db 64 lnhkv 68
 QY 156 VDLKL 160

RESULT 9
 ID W10877 standard; Protein: 157 AA.
 AC W10877;
 DT 25-SEP-1997 (first entry)
 DE TNFL/LT-alpha hybrid.
 KW C-terminal extracellular domain; CD40 ligand; mutated; trimerisation;
 KW lymphotoxin; LT; beta; alpha; tumour necrosis factor; TNF; inhibitor;
 KW signalling; receptor; Fas; treating; autoimmune disease; diabetes;
 KW rheumatoid arthritis; inflammatory bowel disease; HIV proliferation;
 KW immune response; tissue graft.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_difference 13 /note= "LT-alpha subunit association domain residue"
 FT misc_difference 36..38 /note= "LT-alpha subunit association domain residues"
 FT misc_difference 38 /note= "LT-alpha subunit association domain residues"
 FT misc_difference 57..58 /note= "given as O in the specification"
 FT misc_difference 63 /note= "LT-alpha subunit association domain residues"
 FT misc_difference 63 /note= "LT-alpha subunit association domain residue"
 FT misc_difference 95..98 /note= "LT-alpha subunit association domain residues"
 FT misc_difference 97 /note= "LT-alpha subunit association domain residues"
 FT misc_difference 116..117 /note= "given as O in the specification"
 FT misc_difference 117 /note= "LT-alpha subunit association domain residues"

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Query Match      6.8%; Score 115; DB 23; Length 157;  
Best Local Similarity 36.1%; Pred.No. 1.75e+00;  
Matches        26; Conservative    14; Mismatches   26; Indels     6; Gaps       5;
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Dbl          6 rtpsdpaahv-vanpqagqqlwlnrranaflxngvelrdnqlvpseglyfvysguyf 64  
QY           | : | : | : | : | : ||| :|| : ||| :|||| :|  
92 RAPFKKSWAYLQVAKHLNKTLSW-NK--DGIL-HGVRYYDGNLVIQFFGLFYITICLOLF 147
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Dbl         65 kgggcpsthvll 76  
QY          || : | : |  
148 LVQ-CPNNSDVL 158
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RESULT      10  
ID R62470 standard; Protein; 157 AA.  
AC R62470; AC  
DT 05-JUN-1995 (first entry)  
DE Tumour necrosis factor-alpha mutein L75H.  
KW Human; tumour necrosis factor; TNF: TNF-a; expression; mutein; mutation;  
KW receptor; affinity; therapeutic; diagnostic; cancer therapy; cancer;  
KW obesity; septic shock; meningitis.
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OS Synthetic.  
FH Key Location/Qualifiers  
FT FT misc_difference 75 /label= Leu to His  
FT FT  
PN EP-619372-A.  
PD 12-OCT-1994.  
PF 17-MAR-1994; 104154.  
PR 29-WAR-1993: EP-810224.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PI Banner D, Lesslauer W, Lotscher H, Stuber D, Loetscher H;  
PI Steuber, D;  
DR WPI; 94-311810/39.  
DR N-PSDB: O87689.  
PT New human TNF-a muteins with higher affinity for p75-TNFR -  
PT useful e.g. for cancer therapy, treatment of obesity and toxic  
PT shock  
PS Claim 4; Page 15; 53pp; English.
```

RESULT 11
ID R79069 standard; Protein; 179 AA.

ID R79069 standard; Protein; 179 AA.

DE Mouse Fas ligand (partial sequence).

NW Fas cell surface antigen; Fas-L; mouse.
OS Mus musculus.

PD 18-MAY-1995.
PF 10-NOV-1994: .701899.

PR 13-DEC-1993; JP-342526.
 DP 19-MAR-1994; ID-074344

PR 07-SEP-1994; JP-239363.

PA (OSAB-) OSAKA BIOSCIENCE INST

DR WPI; 95-194031/25.
DR N-PSDB: 099498.

PT for treatment a
PS Claim 11. Page

CC which express t

sequence 179

Best Local Similarity 35.

Db 45 ahltnphrsipIewed

UNMCTY TYNTHY AATY DOT YN

156 VDT.KT. 160
:: | ::

```

RESULT 12
ID R88357 standard; Protein; 279 AA.
AC R88357;
DT 15-OCT-1995 (first entry)
DE Mouse Fas ligand.
KW Fas ligand; transplant rejection; autoimmune disease; diabetes;
KW inflammation; graft rejection; rheumatoid arthritis; allergy;
KW cystic fibrosis; multiple sclerosis.
OS Mus musculus.
FH Key Location/Qualifiers
FT peptide 101..279
FT /label= soluble mouse Fas ligand
PN WO9532627-A1.
PD 07-DEC-1995.
PE 26-MAY-1995; U06742.
PR 27-MAY-1994; US-250478.
PR 26-JAN-1995; US-378507.
PA (COLS ) UNIV COLORADO.
PI Bellgrau D, Duke RC;
DR WPI: 96-030252/03.
DR N-PSDB: T09678.
PT Use of Fas ligand - for suppressing lymphocyte-mediated immune
PT responses, e.g. transplant rejection or auto-immune conditions
PS Claim 6; Fig.1; 51pp; English.
CC The expressed protein can be used to suppress and prevent
CC T-lymphocyte-mediated transplant or graft rejection, T-lymphocyte-
CC mediated disease recurrence or to treat T-lymphocyte-mediated
CC diseases. It can be used to treat diabetes, rheumatoid arthritis,
CC multiple sclerosis, cystic fibrosis or allergies.
SQ Sequence 279 AA;

Query Match 6.8%; Score 115; DB 18; Length 279;
Best Local Similarity 35.4%; Pred. No. 1.75e+00;
Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 145 ahltnphrsipledvgtaligvkykkgvlvnetglyfvykvyfrgscnnqp 204
QY 100 AYLOVAKHLNKTLSWVKD-GI-L-HGVRYQDGNLVIFQFGLYFIICQLQLVQ-CPNNS 155
Db 205 lnkv 209
QY 156 VDLKL 160

RESULT 13
ID R77282 standard; Protein; 279 AA.
AC R77282;
DT 05-DEC-1995 (first entry)
DE Mouse Fas-L protein.
KW Fas ligand; Fas-L; cell surface protein; autoimmune disease;
KW self-tolerance.
OS Mus sp.
FH Key Location/Qualifiers
FT domain 1..78
FT /label= Cytoplasmic_domain
FT domain 79..103
FT /label= Transmembrane_domain
FT domain 104..279
FT /label= Extracellular_domain
PN WO9518819-A.
PD 13-JUL-1995.
PE 06-JAN-1995; U00362.
PR 07-JAN-1994; US-179138.
PR 01-FEB-1994; US-190559.
PA (IMV ) IMMUNEX CORP.
PI Goodwin RG;
DR WPI: 95-255032/33.
DR N-PSDB: Q91312.
PT Human and murine DNA encoding ligand(s) binding to cell surface protein
PT Fas - useful for studying auto-immune disorder(s) and development of
PT self-tolerance.
PS Disclosure: Page 29-30; 38pp; English.
CC A cDNA library prepd. from mouse peripheral blood lymphocyte mRNA was

CC screened with a murine Fas-L probe from the 3' end of Fas-L DNA.
CC An isolated clone (Q91312) encoded mouse Fas-L.
SQ Sequence 279 AA;

Query Match 6.8%; Score 115; DB 14; Length 279;
Best Local Similarity 35.4%; Pred. No. 1.75e+00;
Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 145 ahltnphrsipledvgtaligvkykkgvlvnetglyfvykvyfrgscnnqp 204
QY 100 AYLOVAKHLNKTLSWVKD-GI-L-HGVRYQDGNLVIFQFGLYFIICQLQLVQ-CPNNS 155
Db 205 lnkv 209
QY 156 VDLKL 160

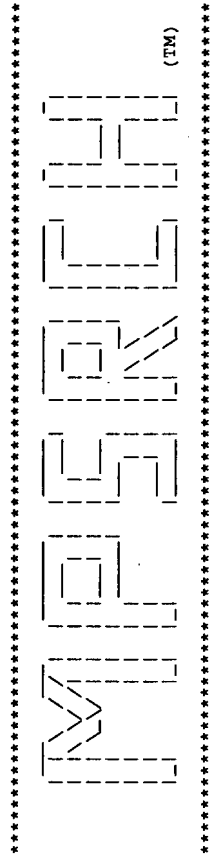
RESULT 14
ID R79098 standard; Protein; 279 AA.
AC R79098;
DT 21-FEB-1996 (first entry)
DE Mouse Fas ligand.
KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; Fas-L; mouse.
OS Mus musculus.
FH Key Location/Qualifiers
FT region 25..78
FT /label= proline-rich
FT domain 79..100
FT /label= transmembrane_anchor
FT /note= "hydrophobic"
FT modified_site 117
FT /label= N-glycosylation_site
FT modified_site 131
FT /label= N-glycosylation_site
FT modified_site 182
FT /label= N-glycosylation_site
FT modified_site 248
FT /label= N-glycosylation_site
FT modified_site 258
FT /label= N-glycosylation_site
PN WO9513293-A1.
PD 18-MAY-1995.
PE 10-NOV-1994; J01899.
PR 10-NOV-1993; JP-305975.
PR 13-DEC-1993; JP-342526.
PR 18-MAR-1994; JP-074344.
PR 08-JUL-1994; JP-180955.
PR 07-SEP-1994; JP-239363.
PR 18-OCT-1994; JP-278378.
PA (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSABA BIOSCIENCE INST.
PI Nagata S, Nakamura N, Suda T, Takahashi T;
DR WPI: 95-194031/25.
DR N-PSDB: Q94156; Q99499.
PT Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto-immune diseases
PS Claim 12; Fig 23-24; 300pp; Japanese.
CC A clone (Q94156) contg. an insert coding for the mouse Fas ligand
CC was isolated using probes derived from a rat Fas-L clone (see
CC Q94153). The mouse sequence contains an open reading frame coding
CC for a 279 amino acid sequence with 5 N-glycosylation sites and a
CC proline-rich region. The deduced mouse amino acid sequence has
CC 91.4% homology with rat Fas-L. Fas ligands are able to induce
CC apoptosis in cells which express the Fas cell surface antigen.
SQ Sequence 279 AA;

Query Match 6.8%; Score 115; DB 14; Length 279;
Best Local Similarity 35.4%; Pred. No. 1.75e+00;
Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 145 ahltnphrsipledvgtaligvkykkgvlvnetglyfvykvyfrgscnnqp 204
QY 100 AYLOVAKHLNKTLSWVKD-GI-L-HGVRYQDGNLVIFQFGLYFIICQLQLVQ-CPNNS 155
Db 205 lnkv 209
QY 156 VDLKL 160

```

search completed: Fri
Job time : 48 secs



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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:44:10 1999; Maspar time 3.93 Seconds
Tabular output not generated. 604.816 Million cell updates/sec

Title: >US-09-079-785-8
Description: (1-234) from US09079785.pep
Perfect Score: 1697
Sequence: 1 MDPGLQALNGMAPPGDTAM.....DTSTPLENVLSFLYNSD 234

Scoring table: PAM 150
Gap 11

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 30.426; Variance 147.499; scale 0.206

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1697	100.0	234	2	US-08-580- Sequence 8, Applicatio	1.39e-136
2	1697	100.0	234	1	US-08-570- Sequence 8, Applicatio	1.39e-136
3	1697	100.0	234	1	US-08-225- Sequence 8, Applicatio	1.39e-136
4	1566	92.3	215	2	US-08-580- Sequence 23, Applicati	4.95e-125
5	1566	92.3	215	1	US-08-225- Sequence 23, Applicati	4.95e-125
6	1566	92.3	215	1	US-08-570- Sequence 23, Applicati	4.95e-125
7	1232	72.6	239	1	US-08-225- Sequence 6, Applicatio	1.17e-95
8	1232	72.6	239	1	US-08-570- Sequence 6, Applicatio	1.17e-95
9	1232	72.6	239	2	US-08-580- Sequence 6, Applicatio	1.17e-95
10	1189	70.1	220	2	US-08-570- Sequence 19, Applicati	6.91e-92
11	1189	70.1	220	2	US-08-580- Sequence 19, Applicati	6.91e-92
12	1189	70.1	220	1	US-08-225- Sequence 20, Applicati	5.06e-62
13	847	49.9	125	2	US-08-580- Sequence 20, Applicati	5.06e-62
14	847	49.9	125	1	US-08-225- Sequence 20, Applicati	5.06e-62
15	847	49.9	125	1	US-08-570- Sequence 21, Applicati	4.98e-44
16	639	37.7	130	2	US-08-580- Sequence 21, Applicati	4.98e-44
17	639	37.7	130	1	US-08-570- Sequence 21, Applicati	4.98e-44
18	639	37.7	130	1	US-08-225- Sequence 21, Applicati	4.98e-44
19	115	6.8	279	3	PCT-US95-0 Sequence 5, Applicatio	6.25e-01
20	112	6.6	156	4	5180811-2 Patent No. 5180811	1.02e-00
21	111	6.5	158	1	US-07-994- Sequence 98, Applicati	1.19e+00
22	110	6.5	161	1	US-07-994- Sequence 61, Applicati	1.40e+00
23	110	6.5	162	1	US-07-994- Sequence 60, Applicati	1.40e+00

24	110	6.5	163	1	US-07-994- Sequence 64, Applicati	1.40e+00
25	111	6.5	281	2	US-08-810- Sequence 2, Applicatio	1.19e+00
26	111	6.5	281	3	PCT-US95-0 Sequence 2, Applicatio	1.19e+00
27	108	6.4	155	1	US-07-994- Sequence 12, Applicati	1.93e+00
28	108	6.4	157	3	PCT-US95-0 Sequence 17, Applicati	1.93e+00
29	108	6.4	157	4	5180811-1 Patent No. 5180811	1.93e+00
30	108	6.4	157	2	US-08-394- Sequence 17, Applicatio	1.93e+00
31	108	6.4	157	1	US-08-041- Sequence 2, Applicatio	1.93e+00
32	108	6.4	158	1	US-07-994- Sequence 86, Applicati	1.93e+00
33	108	6.4	158	1	US-07-994- Sequence 51, Applicati	1.93e+00
34	108	6.4	158	1	US-07-994- Sequence 82, Applicati	1.93e+00
35	108	6.4	158	1	US-08-397- Sequence 10, Applicati	1.93e+00
36	108	6.4	158	1	US-07-794- Sequence 5, Applicatio	1.93e+00
37	108	6.4	158	1	US-07-794- Sequence 7, Applicatio	1.93e+00
38	108	6.4	170	4	5180811-1 Patent No. 5180811	1.93e+00
39	108	6.4	176	4	5180811-12 Patent No. 5180811	1.93e+00
40	108	6.4	177	3	PCT-US95-0 Sequence 21, Applicati	1.93e+00
41	108	6.4	177	2	US-08-394- Sequence 21, Applicati	1.93e+00
42	108	6.4	187	4	5180811-13 Patent No. 5180811	1.93e+00
43	108	6.4	193	2	US-08-889- Sequence 3, Applicatio	1.93e+00
44	108	6.4	233	4	5422425-2 Patent No. 5422425	1.93e+00
45	108	6.4	233	3	PCT-US95-1 Sequence 10, Applicati	1.93e+00

ALIGNMENTS

RESULT 1
ID US-08-580-014-8 STANDARD; PRT; 234 AA.
XX
AC
XX
DT
XX
DE
XX
Sequence 8, Application US/08580014
Sequence 8, Application US/08580014
Patent No. 5753203
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Armitage, Richard J.
APPLICANT: Gruss, Hans-Jurgen
TITLE OF INVENTION: No. 5753203el cytokine That Binds CD30
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Seese, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,014
FILING DATE: 20-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 234 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 234 AA; 26017 MW; 308679 CN;

Query Match 100.0%; Score 1697; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.39e-136;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDPGLQALNGMAPPDGTAMHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVL 60
QY 1 MDPGLQALNGMAPPDGTAMHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVL 60

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QY 61 VVQRTSDIPNSPDNVPKGGNCSEDLICILKRAPFKKSWAYLOVAKHLNKTLSWNKDKGI 120

Db 121 LHGVRYQDGNLVIOFPGLYFIICQLQFLVQCPNNVDLKLELLINKHKKQALVTVCESG 180
QY 121 LHGVRYQDGNLVIOFPGLYFIICQLQFLVQCPNNVDLKLELLINKHKKQALVTVCESG 180

Db 181 MQTKHYQNLSQFLLDYLOVNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234
QY 181 MQTKHYQNLSQFLLDYLOVNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234

RESULT 2
ID US-08-570-923-8 STANDARD; PRT; 234 AA.
XX xxxxxx
AC xxxxxx
DT
XX
DE Sequence 8, Application US/08570923
CC Sequence 8, Application US/08570923
CC Patent No. 5677430
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jürgen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 234 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 234 AA; 26017 MW; 308679 CN;

Query Match 100.0%; Score 1697; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.39e-136;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDPGLQALNGMAPPDGTAMHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVL 60

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QY 61 VVQRTSDIPNSPDNVPKGGNCSEDLICILKRAPFKKSWAYLOVAKHLNKTLSWNKDKGI 120

Db 121 LHGVRYQDGNLVIOFPGLYFIICQLQFLVQCPNNVDLKLELLINKHKKQALVTVCESG 180
QY 121 LHGVRYQDGNLVIOFPGLYFIICQLQFLVQCPNNVDLKLELLINKHKKQALVTVCESG 180

Db 181 MQTKHYQNLSQFLLDYLOVNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234
QY 181 MQTKHYQNLSQFLLDYLOVNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234

RESULT 3
ID US-08-225-989-8 STANDARD; PRT; 234 AA.
XX xxxxxx
AC xxxxxx
DT
XX
DE Sequence 8, Application US/08225989
CC Sequence 8, Application US/08225989
CC Patent No. 5480981
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.

CC	APPLICANT: Gruss, Hans-Jürgen	
CC	TITLE OF INVENTION: NO. 5480981el Cytokine That Binds CD30	
CC	NUMBER OF SEQUENCES: 23	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Kathryn A. Seese, Immunex Corporation	
CC	STREET: 51 University Street	
CC	CITY: Seattle	
CC	STATE: Washington	
CC	COUNTRY: USA	
CC	ZIP: 98101	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	
CC	COMPUTER: Apple Macintosh	
CC	OPERATING SYSTEM: Apple 7.1	
CC	SOFTWARE: Microsoft Word, Version 5.1a	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: US/08/225,989	
CC	FILING DATE: 12 APRIL 1994	
CC	CLASSIFICATION: 435	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 07/966,775	
CC	FILING DATE: 27-OCT-1992	
CC	CLASSIFICATION: 435	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 907,224	
CC	FILING DATE: 01-JUL-1992	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 899,660	
CC	FILING DATE: 15-JUN-1992	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 892,459	
CC	FILING DATE: 02-JUN-1992	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 889,717	
CC	FILING DATE: 26-MAY-1992	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: Seese, Kathryn A.	
CC	REGISTRATION NUMBER: 32,172	
CC	REFERENCE/DOCKET NUMBER: 2804-E	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: (206)587-0430	
CC	TELEFAX: (206)233-0644	
CC	TELEX: 756822	
CC	INFORMATION FOR SEQ ID NO: 8:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 234 amino acids	
CC	TYPE: amino acid	
CC	TOPOLOGY: linear	
CC	MOLECULE TYPE: protein	
CC	SEQUENCE 234 AA; 26017 MW; 308679 CN;	
CC	Query Match 100.0%; Score 1697; DB 1; Length 234;	
CC	Best Local Similarity 100.0%; Pred. No. 1.39e-136;	
CC	Matches 234; Conservative 0; Mismatches 0; Indels 0;	
Db	1 MDPLGQALNGMAPPGDTAMHVPAAGSVASHLGTSTRSYFYLTATLALCLVFTVATIM	
Qy	1 MDPLGQALNGMAPPGDTAMHVPAAGSVASHLGTSTRSYFYLTATLALCLVFTVATIM	
Db	61 VVQRTDSIPNSPNVPLKGCNSEDLLCIUKRAPFKSWAYLOVAKHLNKTKLUSWNRD	
Qy	61 VVQRTDSIPNSPNVPLKGCNSEDLLCIUKRAPFKSWAYLOVAKHLNKTKLUSWNRD	
Db	121 LHGVRYDGNLVIQFPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCE	
Qy	121 LHGVRYDGNLVIQFPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCE	
Db	181 MQTKHVYQNLSQFLLDYQLQWNTTISVNVDTFQYIDTSTFPLENVLSIFLYNSD 234	
Qy	181 MQTKHVYQNLSQFLLDYQLQWNTTISVNVDTFQYIDTSTFPLENVLSIFLYNSD 234	

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US-08-580-014-23          STANDARD;          PRT;   215 AA.
xxxxxx

Sequence 23, Application US/08580014

Sequence 23, Application US/08580014
Patent No. 5753203
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Armitage, Richard J.
APPLICANT: Gruss, Hans-Jurgen
TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Seese, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,014
FILING DATE: 20-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
APPLICATION DATA:
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
APPLICATION DATA:
APPLICATION NUMBER: US 892,459
FILING DATE: 02-JUN-1992
APPLICATION DATA:
APPLICATION NUMBER: US 889,717
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2804-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 215 AA; 24151 MW; 261175 CN;

Query Match          92.3%; Score 1566; DB 2: Length 215;
Best Local Similarity 100.0%; Pred.No. 4.95e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0;

Db      1  MHVPAGSVASHLGTSSRYFLTATLALCLFVTATIMVLVQVTDTSIPNSPDNPL

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QY 20 MHVPAGSVASHLGTTSRSYFLLTATLALCLVETVATIMVLVVQRTDSIPNSPDNVPLKG 79
Db 61 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKGILHGVRVQDGNLVIQFPGLY 120
QY 80 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKGILHGVRVQDGNLVIQFPGLY 139
Db 121 FIICQQLVQCPNNSVDLKLLELLINKHKIKKQALVTVCESGMOTKHVYONLSQFLLDYLQ 180
QY 140 FIICQQLVQCPNNSVDLKLLELLINKHKIKKQALVTVCESGMOTKHVYONLSQFLLDYLQ 199
Db 181 VNTTISVNDTFQYIDTSTFPLENLSIFLYNSD 215
QY 200 VNTTISVNDTFQYIDTSTFPLENLSIFLYNSD 234

RESULT 5
ID US-08-225-989-23 STANDARD; PRT: 215 AA.
XX xxxxxx
DT
DE
DE
DE
XX
CC Sequence 23, Application US/08225989
CC Sequence 23, Application US/08225989
CC Patent No. 5480981
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: NO. 5480981el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822

CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 215 AA; 24151 MW; 261175 CN;
Query Match 92.3%; Score 1566; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.95e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MHVPAGSVASHLGTTSRSYFLLTATLALCLVETVATIMVLVVQRTDSIPNSPDNVPLKG 60
QY 20 MHVPAGSVASHLGTTSRSYFLLTATLALCLVETVATIMVLVVQRTDSIPNSPDNVPLKG 79
Db 61 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKGILHGVRVQDGNLVIQFPGLY 120
QY 80 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKGILHGVRVQDGNLVIQFPGLY 139
Db 121 FIICQQLVQCPNNSVDLKLLELLINKHKIKKQALVTVCESGMOTKHVYONLSQFLLDYLQ 180
QY 140 FIICQQLVQCPNNSVDLKLLELLINKHKIKKQALVTVCESGMOTKHVYONLSQFLLDYLQ 199
Db 181 VNTTISVNDTFQYIDTSTFPLENLSIFLYNSD 215
QY 200 VNTTISVNDTFQYIDTSTFPLENLSIFLYNSD 234

RESULT 6
ID US-08-570-923-23 STANDARD; PRT: 215 AA.
XX xxxxxx
DT
DE
DE
DE
XX
CC Sequence 23, Application US/08570923
CC Sequence 23, Application US/08570923
CC Patent No. 5677430
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 215 AA; 24151 MW; 261175 CN;

Query Match 92.3%; Score 1566; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.95e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MHVPAGSVASHLGTSTRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 60
QY 20 MHVPAGSVASHLGTSTRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 79
Db 61 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKDGILHGVRYQDGNLVQFPGLY 120
QY 80 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKDGILHGVRYQDGNLVQFPGLY 139
Db 121 FIICOLQFLVCPNNSVDLKELELNKIKKQALVTVCESGMQTKHYQNLSQFLLDYLQ 180
QY 140 FIICOLQFLVCPNNSVDLKELELNKIKKQALVTVCESGMQTKHYQNLSQFLLDYLQ 199
Db 181 VNTIISVNDVFQYIDTSTFPLENLSIFLYSNSD 215
QY 200 VNTIISVNDVFQYIDTSTFPLENLSIFLYSNSD 234

RESULT 7
ID US-08-225-989-6 STANDARD; PRT; 239 AA.

XX xxxxxx

Sequence 6, Application US/08225989

Sequence 6, Application US/08225989
Patent No. 5480981

GENERAL INFORMATION:

APPLICANT: Goodwin, Raymond G.

APPLICANT: Smith, Craig A.

APPLICANT: Armitage, Richard J.

APPLICANT: Gruss, Hans-Jurgen

TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Seese, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 239 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 239 AA; 26519 MW; 334382 CN;

Query Match 72.6%; Score 1232; DB 1; Length 239;

Best Local Similarity 70.0%; Pred. No. 1.17e-95;

Matches 168; Conservative 39; Mismatches 26; Indels 7; Gaps 3;

Db 1 MDPGLQAGSCGAPSPDAMQVPGSVASPWSTPWRSTSRYSFYLTATLALCLVFTV 59

QY 1 MDPGLQAGSCGAPSPDAMQVPGSVASPWSTPWRSTSRYSFYLTATLALCLVFTV 54

Db 60 AIIILVYVQKDDSTPNTTEKAPLKGNGSEDLFTCLKSTPKKSWAYLQVSKHLNNTKLS 119

QY 55 ATIMLVVQRTDSIPNSPDNVLPGKNGSEDLICILKRAPFKSWAYLQVAKHLNKTLS 114

Db 120 WNEGTIHLIYQDGNLVQFPGLYFIVCQLQFLVQCSNHSVDLTLQLLINSKIKKQTLV 179

QY 115 WNKDGIHLGVRYQDGNLVQFPGLYFIVCQLQFLVQCPNNSVDLKELELNKIKKQALV 174

Db 180 TVCSGVOSKNIYQNLSQFLHLYQVNSTISYRVNDFQVDTNFTPLDNVLSVFLYSSD 239

QY 175 TVCSGMQTKHYQNLSQFLDLYQVNTISYVNDTFOYIDTSTFPLENLSIFLYSNSD 234

RESULT 8

ID US-08-570-923-6 STANDARD; PRT; 239 AA.

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

XX xxxxxx

CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 239 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 239 AA; 26519 MW; 334382 CN;
Query Match 72.6%; Score 1232; DB 1; Length 239;
Best Local Similarity 70.0%; Pred. No. 1.17e-95;
Matches 168; Conservative 39; Mismatches 26; Indels 7; Gaps 3;
Db 1 MDPGLQAGSCGAPSPDPAMQVQSGVSPWRSTSRFYLTAL-VCLVAV 59
QY 1 MDPGLQALNGMAPPDGTAMHVPAGSVASHL-GT-----TSRSFYLTATLALCLVTV 54
Db 60 AILVLVQKSDPTNTTEKAPLKGNCSEDLCTKTPSKSWAYLQVSKHLNFKLS 119
QY 55 ATIMVLVQRTDIPNSPNVDYFPGLYFICOLQFVQCPNNSVDLKLLELNKHKKQALV 114
Db 120 WNEDGPIHGLIVODGNLIVQFGLYFICOLQFVQCSNHSVDLTQLLNSKIKKQTLV 179
QY 115 WNKGDLHGVGVODGNLIVQFGLYFICOLQFVQCPNNSVDLKLLELNKHKKQALV 174
Db 180 TVCESGVQSKNIQNLSQFLHLLVQNSISVRVDNFQVVDNTFPDLNVLVSFLYSSSD 239
QY 175 TVCESGMQKHVQYNLSQFLDLYQVNTISVNVDTFQIDISTFPLENVLSIFLYNSD 234

RESULT 9
ID US-08-580-014-6 STANDARD; PRT; 239 AA.
XX
AC xxxxxx
XX
DT
XX
DE
XX
Sequence 6, Application US/08580014
XX
Sequence 6, Application US/08580014
CC Patent No. 5753203
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580,014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 239 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 239 AA; 26519 MW; 334382 CN;
Query Match 72.6%; Score 1232; DB 2; Length 239;
Best Local Similarity 70.0%; Pred. No. 1.17e-95;
Matches 168; Conservative 39; Mismatches 26; Indels 7; Gaps 3;

[illegible]

	CC	CLASSIFICATION:	530		
	CC	PRIOR APPLICATION DATA:			
	CC	APPLICATION NUMBER:	US 907,224		
	CC	FILING DATE:	01-JUL-1992		
	CC	PRIOR APPLICATION DATA:			
	CC	APPLICATION NUMBER:	US 899,660		
	CC	FILING DATE:	15-JUN-1992		
	CC	PRIOR APPLICATION DATA:			
	CC	APPLICATION NUMBER:	US 892,459		
	CC	FILING DATE:	02-JUN-1992		
	CC	PRIOR APPLICATION DATA:			
	CC	APPLICATION NUMBER:	US 889,717		
	CC	FILING DATE:	26-MAY-1992		
	CC	ATTORNEY/AGENT INFORMATION:			
	CC	NAME:	Seese, Kathryn A.		
	CC	REGISTRATION NUMBER:	32,172		
	CC	REFERENCE/DOCKET NUMBER:	2804-E		
	CC	TELECOMMUNICATION INFORMATION:			
	CC	TELEPHONE:	(206)587-0430		
	CC	TELEFAX:	(206)233-0644		
	CC	TELEX:	756822		
	CC	INFORMATION FOR SEQ ID NO:	19:		
	CC	SEQUENCE CHARACTERISTICS:			
	CC	LENGTH:	220 amino acids		
	CC	TYPE:	amino acid		
	CC	TOPOLOGY:	linear		
	CC	MOLECULE TYPE:	protein		
	CC	SEQUENCE	220 AA; 24724 MW; 283693 CN;		
	SQ	Query Match	70.1%; Score 1189; DB 2; Length 220;		
		Best Local Similarity	73.8%; Pred. No. 6.9le-92;		
		Matches	149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;		
	Dd	20 STSRSYFYLLSTTAL-VCLVVAVAIILVLVYVKKDSPTNTEKAPLKGNCSEDLFCITLS 78 : : :: : - : :: :- : :: : :: : ::			
	QY	33 TTSRSFYLTATLALCLVTFTATIWLTVVORTDPSNPSPNVPLKGGNCSEDLICILKR 92 : : :: : - : :: :- : :: : :: : ::			
	Dd	79 TPSSKSWAYLVQSKHLNNTKLSWNEBGTIHGLIYODGNLIYQPFGLYFIVCQLFLVQCQS 138 : : :: : - : :: :- :~::~ :~::~ :~::~			
	QY	93 APPKSWAYLVQAKHNLKNKLKSNWKDGILLGVRYQDGNLVIQFPGLYFIICQLFLVQCP 152 : : :: : - : :: :- :~::~ :~::~ :~::~			
	Dd	139 NNSVDTLQLLINSKKTKQTFLTVCESGVSQSKNIYNQLSOFLLHYLOVNSTISVRVDNFQ 198 : : :: : - : :: :- :~::~ :~::~ :~::~			
	QY	153 NNSVDLKLELLINKHKIKQAALTVCESGMQTRKYONLSOFLLDYLQVNTTISVNYDTTFQ 212 : : :: : - : :: :- :~::~ :~::~ :~::~			
	Dd	199 YVDTNTPFDNLVSLVFYSXSD 220 : : :: : - :~::~ :~::~ :~::~			
	QY	213 YIDTSTPFLNVLISFLYSND 234 : : :: : - :~::~ :~::~ :~::~			
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	XX	US-08-225-989-19	STANDARD;	PRT;	220 AA.
	AC	xxxxxx			
	DD				
	DT				
	DX				
	DE				
	XX	Sequence 19, Application US/08225989			
	XX	Sequence 19, Application US/08225989			
	CC	Patent No. 5480981			
	CC	GENERAL INFORMATION:			
	CC	APPLICANT:	Goodwin, Raymond G.		
	CC	APPLICANT:	Smith, Craig A.		
	CC	APPLICANT:	Richtage, Richard J.		
	CC	APPLICANT:	Gross, Hans-Jurgen		
	CC	TITLE OF INVENTION:	No. 5480981el Cytokine That Binds CD30		
	CC	NUMBER OF SEQUENCES:	23		
	CC	CORRESPONDENCE ADDRESS:			
	CC	ADDRESSEE:	Kathryn A. Seese, Immunex Corporation		
	CC	STREET:	51 University Street		
	CC	CITY:	Seattle		
	CC	STATE:	Washington		
	CC				

CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC IMMEDIATE SOURCE:
CC CLONE: huCD30 fragment (PRELIM)
CC SQ SEQUENCE 125 AA; 13767 MW; 89412 CN;

Query Match 49.9%; Score 847; DB 1; Length 125;
Best Local Similarity 93.5%; Pred. No. 5.06e-62;
Matches 116; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Db 1 PGDTVXHVHPAGSEASHLGTTSRXYFYLTTLALCLVFTVATIMLVVQRTDSIPNSPDN 60
QY 15 PGDTAMHVHPAGSVASHLGTTSRXYFYLTTLALCLVFTVATIMLVVQRTDSIPNSPDN 74

Db 61 VPLKGGNCSEDLICILKRAPFKKSWAYLQVKKHLNKTLSWKNKGILHGVRYQDGNLVQ 120
QY 75 VPLKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVQ 134

Db 121 FPGF 124
QY 135 FPGF 138

RESULT 15
ID US-08-570-923-20 STANDARD; PRT; 125 AA.
XX
AC xxxxxx
DT
XX
DE Sequence 20, Application US/08570923
XX
DE Sequence 20, Application US/08570923
CC Patent No. 5677430
CC
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Amitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 125 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein fragment
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC IMMEDIATE SOURCE:
CC CLONE: huCD30 fragment (PRELIM)
CC SQ SEQUENCE 125 AA; 13767 MW; 89412 CN;

Query Match 49.9%; Score 847; DB 1; Length 125;
Best Local Similarity 93.5%; Pred. No. 5.06e-62;
Matches 116; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Db 1 PGDTVXHVHPAGSEASHLGTTSRXYFYLTTLALCLVFTVATIMLVVQRTDSIPNSPDN 60
QY 15 PGDTAMHVHPAGSVASHLGTTSRXYFYLTTLALCLVFTVATIMLVVQRTDSIPNSPDN 74

Db 61 VPLKGGNCSEDLICILKRAPFKKSWAYLQVKKHLNKTLSWKNKGILHGVRYQDGNLVQ 120
QY 75 VPLKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVQ 134

Db 121 FPGF 124
QY 135 FPGF 138

Search completed: Fri Aug 13 16:44:20 1999
Job time : 10 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:41:56 1999; MasPar time 11.68 Seconds
Tabular output not generated.

Title: >US-09-079-785-8
Description: (1-234) from US09079785.pep
Perfect Score: 1697
Sequence: 1 MDPGLQALNGMAPPGDTAM.....DTSTFPLENLSIFLYSNSD 234

Scoring table: PAM 150
Gap 11
Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 45.301; Variance 90.486; scale 0.501

--Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1697	100.0	234	2 A40710	CD30 ligand - human	0.00e+00
2	1232	72.6	239	2 B40710	CD30 ligand - mouse	1.28e-223
3	123	7.2	498	2 S52570	phosphoprotein phosph	5.06e-04
4	117	6.9	499	2 A55346	phosphoprotein phosph	3.54e-03
5	115	6.8	279	2 A53062	Fas ligand - mouse	6.70e-03
6	113	6.7	234	2 JQ1344	tumor necrosis factor	1.26e-02
7	111	6.5	281	2 I38707	Fas ligand - human	2.35e-02
8	108	6.4	233	1 QWHUN	tumor necrosis factor	5.93e-02
9	108	6.4	233	2 S22052	tumor necrosis factor	5.93e-02
10	108	6.4	233	2 D69649	probable long-chain-f	5.93e-02
11	106	6.2	278	2 A49266	fes ligand - rat	1.09e-01
12	104	6.1	232	2 S12606	tumor necrosis factor	1.98e-01
13	100	5.9	379	2 A45443	tubulin--tyrosine lig	6.45e-01
14	98	5.8	185	2 S52715	tumor necrosis factor	1.15e-00
15	98	5.8	233	2 S11688	tumor necrosis factor	8.61e-01
16	98	5.8	233	2 S24642	tumor necrosis factor	1.15e-00
17	99	5.8	568	2 JC5629	Muellerian-inhibiting	8.61e-01
18	98	5.8	619	2 S54636	probable membrane pro	1.15e-00
19	98	5.8	724	2 B71404	hypothetical protein	1.15e-00
20	99	5.8	1684	2 T02632	hypothetical protein	8.61e-01
21	97	5.7	235	2 JU0029	tumor necrosis factor	1.53e-00
22	96	5.7	257	2 C69230	conserved hypothetical	2.03e+00
23	95	5.6	228	2 S67111	hypothetical protein	2.69e-00

24	95	5.6	249	2 S78186	H+-transporting ATP s	2.69e+00
25	95	5.6	879	2 A56277	DNA-directed DNA poly	2.69e+00
26	93	5.5	212	2 S62960	probable membrane pro	4.69e+00
27	94	5.5	281	2 F70700	hypothetical protein	3.55e+00
28	94	5.5	452	2 S72266	translation initiatio	3.55e+00
29	94	5.5	541	2 S42833	F40f12.4 protein - Ca	3.55e+00
30	94	5.5	650	2 S64939	CD45 protein - yeast	3.55e+00
31	93	5.5	2496	2 A71616	secreted protein pfs2	4.69e+00
32	92	5.4	235	1 QWMSN	tumor necrosis factor	6.17e+00
33	92	5.4	249	2 A64510	hypothetical protein	6.17e+00
34	91	5.4	264	2 J77408	phosphoribosylamino	8.10e+00
35	92	5.4	407	2 JQ1654	SFR1 protein - human	6.17e+00
36	92	5.4	720	2 G64230	stringent response-11	6.17e+00
37	90	5.3	749	2 S13518	transposase Tam3 - ga	1.06e+01
38	88	5.2	276	2 B71907	hypothetical protein	1.81e+01
39	88	5.2	287	2 D70225	protein p23 homolog -	1.81e+01
40	88	5.2	301	2 S45880	SC01 protein homolog	1.81e+01
41	88	5.2	309	2 I53384	4-1BB ligand - mouse	1.81e+01
42	88	5.2	471	2 A41680	integral membrane pro	1.81e+01
43	89	5.2	483	2 T01053	hypothetical protein	1.39e+01
44	89	5.2	769	2 S36657	SW16 protein - yeast	1.39e+01
45	89	5.2	808	1 QPNEX	glucose dehydrogenase	1.39e+01

ALIGNMENTS

RESULT 1

ENTRY A40710 #type complete

TITLE CD30 ligand - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-1999

ACCESSIONS A40710

REFERENCE A40710

#authors Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, G.R.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Grabstein, K.H.; Gliniak, B.; McAllister, I.B.; Fanslow, W.; Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, R.J.

#journal Cell (1993) 73:1349-1360

#title CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand defines an emerging family of cytokines with homology to TNF.

#cross-references MUID:93313964

#accession A40710

#status preliminary

#molecule_type mRNA

#residues 1-234 #label SMT

#cross-references GB:L09753; NID:g349277; PID:g349278

KEYWORDS cytokine receptor; membrane protein; surface antigen

SUMMARY #length 234 #molecular-weight 26017 #checksum 1088

Best Match 100.0%; Score 1697; DB 2; Length 234;

Query Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDPGLQALNGMAPPGDTAMHPAGSVASHLGTTSRSYFYLTATLALCLVFTATIMVL 60

QY 1 MDPGLQALNGMAPPGDTAMHPAGSVASHLGTTSRSYFYLTATLALCLVFTATIMVL 60

Db 61 VVQRTDSPNDVPLKGGNCSEDLICILKRAPKFSWAYLQVAKHLNKTLSWNKDG 120

QY 61 VVQRTDSPNDVPLKGGNCSEDLICILKRAPKFSWAYLQVAKHLNKTLSWNKDG 120

Db 121 LHGVRYQDGNLVIPGGLFYFIICQLQFLVQCPNNSVDLKLKLNKIKKQALVTVCES 180

QY 121 LHGVRYQDGNLVIPGGLFYFIICQLQFLVQCPNNSVDLKLKLNKIKKQALVTVCES 180

Db 181 MQTKHVYQNLNLSQFLDYLQVNTTISVNVDTFYIDTSTFFPLENLSIFLYSNSD 234

QY 181 MQTKHVYQNLNLSQFLDYLQVNTTISVNVDTFYIDTSTFFPLENLSIFLYSNSD 234

```

2
RESULT
ENTRY      B40710      #type complete
TITLE      CD30 ligand - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       03-May-1994 #sequence_revision 03-May-1994 #text_change
          17-Mar-1999
ACCESSIONS B40710
REFERENCE   A40710
AUTHORS     Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah,
            T.; Baker, E.; Sutherland, G.R.; Brannan, C.I.; Copeland,
            N.G.; Jenkins, N.A.; Grabstein, K.H.; Gliniak, B.;
            McAllister, I.B.; Fanslow, W.; Alderson, M.; Falk, B.;
            Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage,
            R.J.
JOURNAL     Cell (1993) 73:1349-1360
ENTRY       CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor
TITLE       whose ligand defines an emerging family of cytokines with
            homology to TNF.
KEYWORDS    #cross-references WUID:93313964
SUMMARY     #accession B40710
            ##status preliminary
            ##molecule_type mRNA
            ##residues 1-239 #label SMI
            ##cross-references GB:L09754; NID:G349289
            cytokine receptor; membrane protein; surface antigen
            #length 239 #molecular-weight 26519 #checksum 3403

Query Match 72.6%; Score 1232; DB 2; Length 239;
Best Local Similarity 70.0%; Pred. No. 1.28e-223;
Matches 168; Conservative 39; Mismatches 26; Indels 7; Gaps 3;

Db 1 MDPGLQQAGSCGAPSPDPAMQVQPGSVASPRWRSTPRWRSTSRSTFYLSSTAL-VCLVAV 59
QY 1 MDPGLQQALUNGAMPDGTAMHPAGVASHL-GT-----TSRSFYLTATLALCLVFTV 54

Db 60 AIIILVAVQKDSPTNTTEKAPLKGNGSDDLCTLKSTPSKSKSWAYLVQSKHLNNTKLS 119
QY 55 AIIILVAVQRTDSIPNSPDNPLKGGNGSDDLCTLKRPKPKSWAYLVQAKHLNNTKLS 114

Db 120 WNEDEGTIHLIYQDGNLIVFPFGLYFIVCOLQFLVQCNSHSDVLTQLLINSKIKKOTLV 179
QY 115 WNKDGIHLGVRYQDGNLIVQFPGLYFIICQLQFLVQCNNVDLKLLELNNKHKKQALV 174

Db 180 TVCESGVQSKNIYQNLSOFLHLHYLVQNTSTISVRVDNFQYVDNTFFDLNVLVFLXSSD 239
QY 175 TVCESGMQTKHYVQNLSOFLDLVQNTTISVNDVTFQYIDTFTFPLENLSIFLYNSD 234

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```

3
RESULT      3
ENTRY      S52570      #type complete
TITLE      phosphoprotein phosphatase (EC 3.1.3.16) 5, catalytic subunit
            - human
ALTERNATE_NAMES  serine/threonine phosphatase PP5
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        01-Aug-1995 #sequence_revision 02-Jul-1996 #text_change
            17-Mar-1999
ACCESSIONS  S52570; PC4136
REFERENCE   S52570
            Chen, M.X.; McPartlin, A.E.; Brown, L.; Chen, Y.H.; Barker,
            H.M.; Cohen, P.T.W.
            EMBO J. (1994) 13:4278-4290
            A novel human protein serine/threonine phosphatase, which
            possesses four tetra-tricopeptide repeat motifs and
            localizes to the nucleus.
            #cross-references MUID:95009929
            #accession S52570
            #molecule_type mRNA
            #residues 7-498 #label CH2
            #cross-references EMBL:S73586; EMBL:X89416
            #experimental_source tetratocarcinoma cell line NTERA-2
            PC4136
            Xu, X.L.; Lagercrantz, J.; Zickert, P.; Bajajlica-Lagercrantz,
            #authors
REFERENCE

```

```

S.: Zetterberg, A.
#journal Biochem. Biophys. Res. Commun. (1996) 218:514-517
#title Chromosomal localization and 5' sequence of the human protein in
serine/threonine phosphatase 5' gene.
#accession PC4136
#molecule_type mRNA
##residues 1-37 #label XUX
##cross-references EMBL:X92121; NID:g1177477; PID:e205526; PID:g1177478
##experimental_source fetal brain
GENETICS
#gene GDB:PPP5C; PPP5; PP5
#map_position 19q13.3-19q13.3
#description catalyzes the hydrolytic dephosphorylation of
protein-phosphoserine and protein-phosphothreonine
plays a role in the regulation of RNA synthesis and mitosis
CLASSIFICATION
#note #superfamily phosphoprotein phosphatase homology;
phosphoserine core homology; tetratricopeptide repeat
homology
KEYWORDS
#iron; nucleus; phosphoric monoester hydrolase; zinc
FEATURE
#domain tetratricopeptide repeat homology #label Ttr1\
62-61 #domain tetratricopeptide repeat homology #label Ttr2\
28-95 #domain tetratricopeptide repeat homology #label Ttr3\
96-129 #domain phosphoprotein phosphatase homology #label PPP\
204-467 #domain phosphoserine core homology #label PC\
236-305 #binding_site iron (Asp, His, Asp) #status predicted\
242,244,271 #binding_site zinc (Asp, Asn, His, His) #status
271,303,352,426 predicted\
274,304,450 #active_site Asp, His, Tyr #status predicted\
275,399 #binding_site substrate phosphate (Arg) #status
predicted
SUMMARY
#length 498 #molecular_weight 56820 #checksum 5353
Query Match 7.2%; Score 123; DB 2; Length 498;
Best Local Similarity 26.1%; Pred. No. 5.06e-04;
Matches 23; Conservative 28; Mismatches 31; Indels 6; Gaps 6;
Db 208 CAQILYQV-KEVLS-KLSTVETLTKETKITVC-GDTHG-QFYDLLNIFELGSPSET 263
QY 143 CQQLFVQCPSNVDKLELLNKHKKQALVTCESGMQKHVYQNLSQFLLDYQVNT 202
: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 264 NPXI-FNG-DFVDRGFSVEVILTFGF 289
QY 203 TISVNDTFQYIDTFPLENVLSIFLY 230
: : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 4
ENTRY #type complete
TITLE phosphoprotein phosphatase (EC 3.1.3.16) ppt - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change
17-Mar-1999
ACCESSIONS A55346
REFERENCE A55346
#authors Becker, W.; Kentrup, H.; Klumpp, S.; Schultz, J.E.; Joost,
H.G.
#journal J. Biol. Chem. (1994) 269:22586-22592
#title Molecular cloning of a protein serine/threonine phosphatase
containing a putative regulatory tetratricopeptide repeat
domain.
#cross-references MIM:14357899
#accession A55346
##status preliminary
##molecule_type mRNA
##residues 1-499 #label BEC
##cross-references GB:X7237
##note authors translated the codon AAG for residue 53 as Gln,
and GGA for residue 496 as Leu
CLASSIFICATION
#superfamily phosphoprotein phosphatase homology;
phosphoserine core homology; tetratricopeptide repeat
homology

```

[illegible]

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#accession I38554
##status preliminary: translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-281 ##label RE2
##cross-references EMBL:U08137; NID:9624627; PID:9624628
GENETICS
#gene FasL
#introns 151/1; 116/3
#glycoprotein: transmembrane protein
KEYWORDS
#domain transmembrane #status predicted #label TMN
#binding_site carbohydrate (Asn) (covalent) #status
#predicted
SUMMARY
#length 281 #molecular-weight 31485 #checksum 3826
Query Match 6.5% Score 111; DB 2; Length 281;
Best Local Similarity 40.4%; Pred.No. 2.35e-02;
Matches 21; Conservative 7; Mismatches 20; Indels 4; Gaps 3;
Db 160 LEWEDTYGIVLLSGVKRGGVLINETGLTYFYKVFYRGQSNLPLSHKV 211
| | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 113 LSNKDG-GI--LHGVRQDGNLVQIFPGLYFIICQLQLVQ-CPNNSVDLKL 160
RESULT 8
ENTRY QWHUN #type complete
TITLE tumor necrosis factor alpha precursor - human
ALTERNATE_NAMES cachectin; TNF alpha
ORGANISM #formal_name Homo sapiens #common_name man
DATE 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
26-Feb-1999
ACCESSIONS A93585; S36153; A93351; A44189; B61478; I53311; S62610;
A01646; B23784
REFERENCE A93585
#authors Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.;
Jarrett-Nedwin, J.; Pennica, D.; Goeddel, D.V.; Gray, P.W.
#journal Nucleic Acids Res. (1985) 13:6361-6373
#title Human lymphotoxin and tumor necrosis factor genes: structure,
homology and chromosomal localization.
#cross-references MUID:86016093
#accession A93585
##molecule_type DNA
##residues 1-233 ##label NED
##cross-references GB:X02910; GB:X02159; NID:g37209; PID:g37210
REFERENCE S36152
#authors Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.;
Primas, G.; Perrot, V.; Jurka, J.; Rodriguez-Tome, P.;
Claverie, J.M.; Dausset, J.; Cohen, D.
#journal Nature Genet. (1993) 3:137-145
#title Dense Alu clustering and a potential new member of the
NFkappaB family within a 90 kilobase HLA class III segment.
#accession S36153
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-233 ##label IRI
##cross-references EMBL:Z15026; NID:g37211; PID:g37212
#note the nucleotide sequence was submitted to the EMBL Data
Library, August 1992
REFERENCE A93351
#authors Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.;
Derynck, R.; Palladino, M.A.; Kohr, W.J.; Aggarwal, B.B.;
Goeddel, D.V.
#journal Nature (1984) 312:724-729
#title Human tumor necrosis factor: precursor structure, expression
and homology to lymphotoxin.
#cross-references MUID:85086244
#accession A93351
##molecule_type mRNA
##residues 1-233 ##label PEN
#note this protein was isolated from the monocyte-like cell
line HL-60 from a promyelocytic leukemia
REFERENCE A44189
#authors Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.;

```

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#journal Strickler, J.; Van Arsdel, J.N.; Yamamoto, R.; Mark, D.F.
Science (1985) 228:149-154
#title Molecular cloning of the complementary DNA for human tumor
necrosis factor.
#cross-references MUID:85142190
#accession A44189
##molecule_type mRNA
##residues 1-62,'S',64-233 ##label WAN
##cross-references GB:M10988; NID:g339737; PID:g339738
REFERENCE A61478
#authors Fukuda, S.; Ando, S.; Sanou, O.; Tani, M.; Fujii, M.;
Masaki, N.; Nakamura, K.I.; Ando, O.; Torigoe, K.;
Sugimoto, T.; Kurimoto, M.
#journal Lymphokine Res. (1988) 7:175-185
#title Simultaneous production of natural human tumor necrosis
factor-alpha, -beta and interferon-alpha from BALL-1 cells
stimulated by HVJ.
#accession B61478
##molecule_type protein
##residues 83-102;109-119;121-128,'X',130-131;142-144,'X',146,
'XXX',150-152;159-174;180,'X',182-204 ##label FUK
REFERENCE A92511
#authors Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer,
S.A.; Henzel, W.J.; Bringman, T.S.; Nedwin, G.E.; Goeddel,
D.V.; Harkins, R.N.
#journal J. Biol. Chem. (1985) 260:2345-2354
#title Human tumor necrosis factor. Production, purification, and
characterization.
#cross-references MUID:85130974
#contents annotation: disulfide bond
REFERENCE I53311
#authors Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden,
J.; Tizard, R.; Kawashima, E.; Shaw, A.; Johnson, M.
#journal Eur. J. Biochem. (1985) 152:515-522
#title Molecular cloning and expression of human tumor necrosis
factor and comparison with mouse tumor necrosis factor.
#cross-references MUID:86030296
#accession I53311
##status translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-233 ##label RES
##cross-references GB:M26331; NID:g339763; PID:g339764
##experimental_source U-937 cells
REFERENCE S62610
#authors Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
#journal Eur. J. Biochem. (1996) 235:431-437
#title O-Glycosylated species of natural human tumor-necrosis
factor-alpha.
#cross-references MUID:96202967
#accession S62610
##status preliminary
##molecule_type protein
##residues 77-99 ##label TAK
COMMENT Secreted from mitogen-activated macrophages within 4-24 hours after
induction, TNF-alpha can cause cytolysis of certain tumor cell
lines and have an antiproliferative effect on others without
detriment to normal cells. It can also act synergistically with
interferon gamma to kill certain transformed cell lines.
COMMENT TNF-alpha and -beta (lymphotoxin) are the products of different
genes closely linked on chromosome 6. They are induced by similar
mitogenic stimuli and have similar biological activities but are
produced by different cell types and have different induction
kinetics.
GENETICS
#gene GDS:TNF; TNFA
#cross-references GDB:I20441; OMIM:191160
#map_position 6p21.3-6p21.3
#introns 62/3; 78/1; 94/1
CLASSIFICATION cytokine; cytotoxin; glycoprotein; lymphokine; macrophage;
membrane protein
KEYWORDS
FEATURE 77-233
#product tumor necrosis factor #status experimental

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[illegible]

[illegible]

QY 122 HGVRYODGNLVIOFPGLYFIICQLQLVQ-CPNNSV 156

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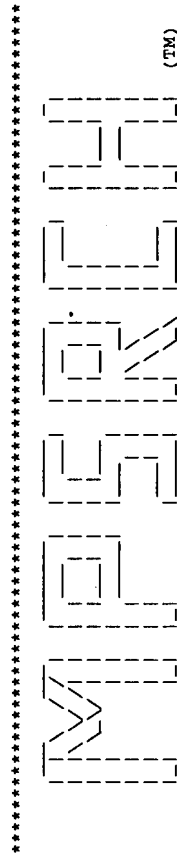
RESULT 15
ENTRY S11688 #type complete
TITLE tumor necrosis factor alpha - cat
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
08-Sep-1997
ACCESSIONS S11688
REFERENCE S11688
#authors McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.;
Rawlings, C.A.
#journal Nucleic Acids Res. (1990) 18:5563
#title Gene sequence of feline tumor necrosis factor alpha.
#cross-references MUID:91016860
#accession S11688
#status preliminary
##molecule_type DNA
##residues 1-233 #label MCG
##cross-references EMBL:X54000; NID:g1084; PID:g295777
GENETICS
#introns 62/3; 78/1; 94/1
CLASSIFICATION #superfamily tumor necrosis factor
KEYWORDS transmembrane protein
SUMMARY #length 233 #molecular-weight 25322 #checksum 5607

Query Match 5.8%; Score 99; DB 2; Length 233;
Best Local Similarity 36.7%; Pred. No. 8.61e-01;
Matches 18; Conservative 10; Mismatches 19; Indels 2; Gaps 2;

Db 104 RLSRRANALLANGVELTDNOLKVPDGLYLIYSQVLFYGGGCPSTHVL 152
:|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
QY 112 KLSWNKDGL-HGVRYODGNLVIOFPGLYFIICQLQLVQ-CPNNSVDL 158

```

Search completed: Fri Aug 13 16:42:17 1999
Job time : 21 secs.



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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Aug 13 16:42:33 1999; MasPar time 8.14 Seconds
Tabular output not generated.

Title: >US-09-079-785-8
Description: (1-234) from US09079785.pep
Perfect Score: 1697
Sequence: 1 MDPGLOALNGVAPGDTAM.....DSTFPLENVLSIFLYNSD 234

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 46.418; Variance 79.389; scale 0.585

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Query Match	Length	ID	Description	Pred. No.		
1	1697	100.0	234	1 CD3L_HUMAN CD30 LIGAND (CD30-L) (0.00e+00		
2	1232	72.6	239	1 CD3L_MOUSE CD30 LIGAND (CD30-L).	9.13e-261		
3	123	7.2	499	1 PPP5_HUMAN SERINE/THREONINE PROTE	3.82e-05		
4	117	6.9	499	1 PPP5_RAT SERINE/THREONINE PROTE	3.55e-04		
5	115	6.8	279	1 FASL_MOUSE FAS ANTIGEN LIGAND.	7.36e-04		
6	113	6.7	234	1 TNFA_MOUSE TUMOR NECROSIS FACTOR	1.51e-03		
7	110	6.5	233	1 TNFA_MACMU TUMOR NECROSIS FACTOR	4.40e-03		
8	111	6.5	281	1 FASL_HUMAN FAS ANTIGEN LIGAND (AP	3.09e-03		
9	108	6.4	233	1 TNFA_HUMAN TUMOR NECROSIS FACTOR	8.88e-03		
10	108	6.4	233	1 TNFA_PAPSP TUMOR NECROSIS FACTOR	8.88e-03		
11	108	6.4	560	1 LFA3_BACSU LONG-CHAIN-FATTY-ACID-	8.88e-03		
12	106	6.2	233	1 TNFA_PAPHU TUMOR NECROSIS FACTOR	1.78e-02		
13	106	6.2	278	1 FASL_RAT FAS ANTIGEN LIGAND.	1.78e-02		
14	104	6.1	232	1 TNFA_PIG TUMOR NECROSIS FACTOR	3.52e-02		
15	103	6.1	233	1 TNFA_MACFA TUMOR NECROSIS FACTOR	4.94e-02		
16	102	6.0	233	1 TNFA_CANFA TUMOR NECROSIS FACTOR	6.92e-02		
17	101	6.0	2670	1 YAQ5_SCHPO PUTATIVE TRANSLATIONAL	9.56e-02		
18	100	5.9	379	1 TTL_PIG TUBULIN--TYROSINE LIGA	1.35e-01		
19	98	5.8	229	1 TNFA_CEREL TUMOR NECROSIS FACTOR	2.60e-01		
20	99	5.8	233	1 TNFA_FELCA TUMOR NECROSIS FACTOR	1.87e-01		
21	98	5.8	233	1 TNFA_BOVIN TUMOR NECROSIS FACTOR	2.60e-01		
22	97	5.7	235	1 TNFA_RAT TUMOR NECROSIS FACTOR	3.59e-01		
23	97	5.7	377	1 TTL_BOVIN TUBULIN--TYROSINE LIGA	3.59e-01		

24	93	5.5	79	1	YF71_HA8IN	HYPOTHETICAL PROTEIN H	1.28e+00
25	93	5.5	212	1	YND8_YEAST	HYPOTHETICAL 24.7 KD P	1.28e+00
26	93	5.5	291	1	TRAI_MOUSE	TNF-RELATED APOPTOSIS	1.28e+00
27	94	5.5	452	1	E2BG_RAT	TRANSILATION INITIATION	9.35e-01
28	94	5.5	650	1	CC45_YEAST	CELL DIVISION CONTROL	9.35e-01
29	92	5.4	235	1	TNFA_MOUSE	TUMOR NECROSIS FACTOR	1.75e+00
30	92	5.4	249	1	YZ01_METJA	HYPOTHETICAL PROTEIN M	1.75e+00
31	92	5.4	375	1	GM12_SCHPO	ALPHA-1,2-GALACTOSYLTR	1.75e+00
32	92	5.4	436	1	VU10_HSV6U	UIO PROTEIN.	1.75e+00
33	92	5.4	720	1	SPOT_MYCGE	PROBABLE GUANOSINE-3',	1.75e+00
34	89	5.2	234	1	TNFA_CAVPO	TUMOR NECROSIS FACTOR	4.37e+00
35	88	5.2	301	1	SC02_YEAST	SC02 PROTEIN PRECURSOR	5.89e+00
36	88	5.2	309	1	41BL_MOUSE	4-1BB LIGAND (4-1BBL).	5.89e+00
37	88	5.2	382	1	Y753_HA8IN	HYPOTHETICAL PROTEIN H	5.89e+00
38	88	5.2	471	1	PSS1_CRIL0	PHOSPHATIDYL SERINE SYN	5.89e+00
39	88	5.2	473	1	PSS1_MOUSE	PHOSPHATIDYL SERINE SYN	5.89e+00
40	88	5.2	531	1	TCPY_MOUSE	T-COMPLEX PROTEIN 1, Z	5.89e+00
41	88	5.2	678	1	GARP_PLAFF	GLUTAMIC ACID-RICH PRO	5.89e+00
42	89	5.2	769	1	SWIG_KLU0A	REGULATORY PROTEIN SWI	4.37e+00
43	89	5.2	808	1	DHG_GLOOX	GLUCOSE DEHYDROGENASE	4.37e+00
44	88	5.2	1189	1	PTNE_MOUSE	PROTEIN-TYROSINE PHOSP	5.89e+00
45	88	5.2	1202	1	YE01_SCHPO	HYPOTHETICAL 138.5 KD	5.89e+00

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	234 AA.
ID	CD3L_HUMAN			
AC	P32971;			
DT	01-OCT-1993 (REL. 27, CREATED)			
DT	01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)			
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)			
DE	CD30 LIGAND (CD30-L) (CD153 ANTIGEN).			
GN	CD30LG OR CD30L.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
RC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.			
RP	[1]			
RA	SEQUENCE FROM N.A.			
RA	MEDLINE; 93313964.			
RA	SMITH C.A., GRUES H.-J., DAVIS T., ANDERSON D., FARRAH T.,			
RA	BAKER E., SUTHERLAND G.R., BRANNAN C.I., COPELAND N.G., JENKINS N.A.,			
RA	GRASSTEIN K.H., GLINKA B., MCALISTER I.B., FANSLAW W., ALDERSON M.,			
RA	FALK B., GIMSELS S., GILLIS S., DIN W.S., GOODWIN R.G., ARMITAGE R.J.;			
RT	"CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose			
RT	ligand defines an emerging family of cytokines with homology to			
RT	TNF."			
RL	CELL 73:1349-1360(1993).			
CC	-1- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF			
CC	T CELLS.			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			
CC	-1- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd153.htm"			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; L09753; G349278; -			
DR	PIR; A40710; A40710.			
DR	PROSITE; PS00251; TNF_1; 1.			
DR	PROSITE; PS50049; TNF_2; 1.			
DR	PFAM; PF00229; TNF; 1.			
KW	CD30; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.			
FT	DOMAIN 1 37			
FT	TRANSMEM 38 62			
FT	DOMAIN 63 234			
FT	CARBOHYD 81 81			

POTENTIAL.

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

EXTRACELLULAR (POTENTIAL).

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FT CARBOHYD 109 109 POTENTIAL.
FT CARBOHYD 153 153 POTENTIAL.
FT CARBOHYD 189 189 POTENTIAL.
FT CARBOHYD 201 201 POTENTIAL.
SQ SEQUENCE 234 AA: 26017 MW; A77E97B1 CRC32;
Query Match 100.0%; Score 1697; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MDPGLQALNGHAPPDGTAMHPVAGSVASHLGTTSRSYFLTTATLALCLVFTVATIMVL 60
QY 1 MDPGLQALNGHAPPDGTAMHPVAGSVASHLGTTSRSYFLTTATLALCLVFTVATIMVL 60
Db 61 VVQRTDSIPNSPDNVLKGGNCSEDLCLILKRAPFKSWAYLQVAKHLNKLWNKDKI 120
QY 61 VVQRTDSIPNSPDNVLKGGNCSEDLCLILKRAPFKSWAYLQVAKHLNKLWNKDKI 120
Db 121 LHGVRYODGNLVIOFPGLYFIICQLQFLVQCPNNSVDLKLLELNKHIKKQALVTVCESS 180
QY 121 LHGVRYODGNLVIOFPGLYFIICQLQFLVQCPNNSVDLKLLELNKHIKKQALVTVCESS 180
Db 181 MOTKHVYQNLSEFLDYLQVNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 234
QY 181 MOTKHVYQNLSEFLDYLQVNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 234
RESULT 2
ID CD3L_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE CD30 LGAND (CD30-L).
GN CD30LG OR CD30L.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-T-CELL;
RA SMITH C.A., GRUEN H.-J., DAVIS T., ANDERSON D., FARRAH T.,
RA BAKER E., SUTHERLAND G.R., BRANNAN C.I., COPELAND N.G., JENKINS N.A.,
RA GRABSTEIN K.H., GLINKA B., MCALISTER I.B., FANSLAW W.G., ALDERSON M.,
RA FALK B., GIMPEL S., GILLIS S., DIN W.S., GOODWIN R.G., ARMITAGE R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF.";
RL CELL 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; L09754; G349289; -
DR PIR; B40710; B40710.
DR MGD; MGI:88328; CD30L.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR PFAM; PF00229; TNF; 1.
DR CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
FT DOMAIN 1 43
FT SIGNAL-ANCHOR (POTENTIAL).
FT TRANSMEM 44 67
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 58 239
FT EXTRACELLULAR (POTENTIAL).
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FT CARBOHYD 75 75 POTENTIAL.
FT CARBOHYD 86 86 POTENTIAL.
FT CARBOHYD 114 114 POTENTIAL.
FT CARBOHYD 158 158 POTENTIAL.
FT CARBOHYD 194 194 POTENTIAL.
FT CARBOHYD 206 206 POTENTIAL.
SQ SEQUENCE 239 AA: 26519 MW; 1EB8A11D CRC32;
Query Match 72.6%; Score 1232; DB 1; Length 239;
Best Local Similarity 70.0%; Pred. No. 9.13e-261;
Matches 168; Conservative 39; Mismatches 26; Indels 7; Gaps 3;
Db 1 MDPGLQALNGHAPPDGTAMHPVAGSVASHLGTTSRSYFLTTATLALCLVFTVATIMVL 59
QY 1 MDPGLQALNGHAPPDGTAMHPVAGSVASHLGTTSRSYFLTTATLALCLVFTVATIMVL 59
Db 60 AILVLVQKSTNTTEKAPLKGNCSEDLCTLKSTPKSKSWAYLQVSKHLNNTKLS 119
QY 55 ATIMVLVQRTDSIPNSPDNVLKGGNCSEDLCLILKRAPFKSWAYLQVAKHLNNTKLS 114
Db 120 WNEGTGRIHGLIYODGNLVIOFPGLYFIICQLQFLVQCPNNSVDLKLLELNKHIKKQALV 179
QY 115 WNEGTGRIHGLIYODGNLVIOFPGLYFIICQLQFLVQCPNNSVDLKLLELNKHIKKQALV 174
Db 180 TVCESGVQSKNIYQNLSEFLDYLQVNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 239
QY 175 TVCESGVQSKNIYQNLSEFLDYLQVNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 234
RESULT 3
ID PPP5_HUMAN STANDARD; PRT; 499 AA.
AC P5041; Q16722;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.1.3.16) (PP5) (PROTEIN
DE PHOSPHATASE T) (PP-T) (PPT).
GN PPP5C OR PPP5
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE OF 7-499 FROM N.A.
RX MEDLINE; 95009929.
RA CHEN M.X., MCPARTLIN A.E., BROWN L., CHEN Y.H., BARKER H.M.,
RA COHEN P.T.W.;
RT "A novel human protein serine/threonine phosphatase, which possesses
RT four tetraatricopeptide repeat motifs and localizes to the nucleus.";
RL EMBO J. 13:4278-4290(1994).
RN [2]
RP SEQUENCE OF 9-499 FROM N.A.
RC TISSUE-FETAL BRAIN;
RX MEDLINE; 96115607.
RA YONG W.H., UERI K., CHOU D., REEVES S.A., VON DEIMLING A.,
RA GUSELLA J.F., MOHREWEISER H.W., BUCKLER A.J., LOUIS D.N.;
RT "Cloning of a highly conserved human protein serine-threonine
RT phosphatase gene from the glioma candidate region on chromosome
RL 19q13.3";
RN [3]
RP GENOMICS 29:533-536(1995).
RC SEQUENCE OF 1-37 FROM N.A.
RX TISSUE-FETAL BRAIN;
RX MEDLINE; 96144708.
RA XU X., LAGERCRANTZ J., ZICKERT P., BAJALICA-LAGERCRANTZ S.,
RA ZETTERBERG A.;
RT "Chromosomal localization and 5' sequence of the human protein
RT serine/threonine phosphatase 5' gene.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 218:514-517(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS) OF 19-177.
RX MEDLINE; 98151343.
RA DAS A.K., COHEN P.W., BARFORD D.;
RT "The structure of the tetraatricopeptide repeats of protein
```

```

RT phosphatase 5; implications for TPR-mediated protein-protein
RL interactions."
CC EMBO J. 17:1192-1199(1998).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF RNA BIOGENESIS
CC AND/OR MITOSIS. IN VITRO, DEPHOSPHORYLATES SERINE RESIDUES OF
CC SKELETAL MUSCLE PHOSPHORYLASE AND HISTONE H1.
CC -1- SUBCELLULAR LOCATION: NUCLEAR; PREDOMINANTLY, BUT ALSO PRESENT IN
CC THE CYTOPLASM.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 3 TPR DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-T
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; X89416; G897761;
DR EMBL; U25174; G112931;
DR EMBL; X92121; E20526;
DR PDB; 1A17; 29-APR-98.
DR MM; 600658;
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
DR PFAM; PF00149; Stphosphatase; 1.
DR PFAM; PF00515; TPR; 2.
DR KW HYDROLASE; IRON; MANGANESE; NUCLEAR PROTEIN; REPEAT; TPR DOMAIN;
KW 3D-STRUCTURE. 28 61 TPR 1.
FT REPEAT 62 95 TPR 2.
FT REPEAT 96 129 TPR 3.
FT DOMAIN 184 492 CATALYTIC.
FT METAL 242 242 IRON (BY SIMILARITY).
FT METAL 244 244 IRON (BY SIMILARITY).
FT METAL 271 271 IRON AND MANGANESE (BY SIMILARITY).
FT METAL 303 303 MANGANESE (BY SIMILARITY).
FT ACT_SITE 304 304 GENERAL ACID (BY SIMILARITY).
FT METAL 352 352 MANGANESE (BY SIMILARITY).
FT METAL 427 427 MANGANESE (BY SIMILARITY).
FT CONFLICT 403 403 S -> T (IN REF. 2).
SQ SEQUENCE 499 AA; 56878 MW; 7D584278 CRC32;

Query Match 7.28; Score 123; DB 1; Length 499;
Best Local Similarity 26.18; Pred. No. 3.82e-05;
Matches 23; Conservative 28; Mismatches 31; Indels 6; Gaps 6;

Db 208 CAYOILVQV-KEVLS-KLSLTVETTLKETEKITVC-CDTHG-QFYDLLNIFELNGLPSET 263
QY 143 CQQLFLVQCPNNSVDL-KLELLINKHKQALVTVCESGMQTKHYVQNLSQFLLDYLVQNT 202
Db 264 NPVI-FNG-DFVDRGFSFVEIITLFGF 289
QY 203 TISVNDTFQYIDTSTFPLENLSIFLY 230

RESULT 4
ID PPP5_RAT STANDARD; PRT; 499 AA.
AC P53042;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN
DE PHOSPHATASE T) (PPT).
GN PPP5C.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RT STRAIN-SPRAGUE-DAWLEY; TISSUE-TESTIS;

phosphatase 5; implications for TPR-mediated protein-protein
interactions."
EMBO J. 17:1192-1199(1998).
-1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF RNA BIOGENESIS
AND/OR MITOSIS. IN VITRO, DEPHOSPHORYLATES SERINE RESIDUES OF
SKELETAL MUSCLE PHOSPHORYLASE AND HISTONE H1.
-1- SUBCELLULAR LOCATION: NUCLEAR; PREDOMINANTLY, BUT ALSO PRESENT IN
THE CYTOPLASM.
-1- TISSUE SPECIFICITY: UBIQUITOUS.
-1- SIMILARITY: CONTAINS 3 TPR DOMAINS.
-1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-T
SUBFAMILY.
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EMBL; X89416; G897761;
EMBL; U25174; G112931;
EMBL; X92121; E20526;
PDB; 1A17; 29-APR-98.
MM; 600658;
PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
PFAM; PF00149; Stphosphatase; 1.
PFAM; PF00515; TPR; 2.
KW HYDROLASE; IRON; MANGANESE; NUCLEAR PROTEIN; REPEAT; TPR DOMAIN;
KW 3D-STRUCTURE. 28 61 TPR 1.
FT REPEAT 62 95 TPR 2.
FT REPEAT 96 129 TPR 3.
FT DOMAIN 184 492 CATALYTIC.
FT METAL 242 242 IRON (BY SIMILARITY).
FT METAL 244 244 IRON (BY SIMILARITY).
FT METAL 271 271 IRON AND MANGANESE (BY SIMILARITY).
FT METAL 303 303 MANGANESE (BY SIMILARITY).
FT ACT_SITE 304 304 GENERAL ACID (BY SIMILARITY).
FT METAL 352 352 MANGANESE (BY SIMILARITY).
FT METAL 427 427 MANGANESE (BY SIMILARITY).
FT CONFLICT 403 403 S -> T (IN REF. 2).
SQ SEQUENCE 499 AA; 56878 MW; 7D584278 CRC32;

Query Match 6.9%; Score 117; DB 1; Length 499;
Best Local Similarity 28.18; Pred. No. 3.55e-04;
Matches 25; Conservative 27; Mismatches 29; Indels 8; Gaps 8;

Db 208 CAYOILVQV-KE-V-LCKSLTVETTLKETEKITVC-GDTHG-QFYDLLNIFELNGLPSE 262
QY 143 CQQLFLVQCPNNSVDL-KLELLINKHKQALVTVCESGMQTKHYVQNLSQFLLDYLVQV 201
Db 263 TNPI-FNG-DFVDRGFSFVEIITLFGF 289
QY 202 TISVNDTFQYIDTSTFPLENLSIFLY 230

RESULT 5
ID FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE FAS ANTIGEN LIGAND.
GN APTLGI OR FASL OR GLD.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX TAKAHASHI T., TANAKA M., BRANNAN C.I., JENKINS N.A., COPELAND N.G.,
RA SUDA T., NAGATA S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
mutation in the Fas ligand."

```

CELL 76:969-976(1994).

[2]
RN SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELLING.
RP STRAIN=C57BL/6;
RX MEDLINE: 95388076.
RA PEITSCH M.J., TSCHOPP J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
of the TNF family."
RL MOL. IMMUNOL. 32:761-772(1995).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE: 95196085.
RA LYNCH D.H., WATSON M.L., ALDERSON M.R., BAUM P.R., MILLER R.E.,
RA TOUGH T., GIBSON M., DAVIS-SMITH T., SMITH C.A., HUNTER K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
TNF family gene cluster."
RL IMMUNITY 1:131-136(1994).
RN [4]
RN CHARACTERIZATION OF VARIANT GLD.
RP MEDLINE: 96091792.
RA HAHNE M., PEITSCH M.C., IRMLER M., SCHROETER M., LOWIN B.,
RA ROUSSEAU M., BRON C., RENNO T., FRENCH L., TSCHOPP J.;
RT "Characterization of the non-functional Fas ligand of gld mice."
RL INT. IMMUNOL. 7:1381-1386(1995).
CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
T CELLS, OR BOTH.
CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
SURFACE.
CC -!- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U06948; G473565; -
DR EMBL: U10984; G511222; -
DR EMBL: S76752; G913760; -
DR MGD: MGI:92255; FASL.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR PFAM: PF00229; TNF; 1.
DR HSP: P01375; 2TUN.
KW CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR; APOPTOSIS;
KW DISEASE MUTATION.
FT DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 4 69 PRO-RICH.
FT DOMAIN 45 51 POLY-PRO.
FT DISULFID 200 231 BY SIMILARITY.
FT VARIANT 273 F -> L (IN GLD; ABOLISH BIDDING OF FASL TO
ITS RECEPTOR).
FT CARBOHYD 117 117 POTENTIAL.
FT CARBOHYD 182 182 POTENTIAL.
FT CARBOHYD 248 248 POTENTIAL.
FT CARBOHYD 258 258 POTENTIAL.
SQ SEQUENCE 279 AA; 31442 MW; AFD84D4B CRC32;

Query Match 6.8%; Score 115; DB 1; Length 279;
Best Local Similarity 35.4%; Pred. No. 7.36e-04;

Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 145 AHLTGNPHSRISPLEWEDTYGTALISGVKYGKGLVNETGLYFYVYFVGQSCNNOP 204
QY 100 AYLOQVAKHLNKLKLSWKN-D-GI-L-HGVRYODGNLVIOFPGLYFIICQLQLVQ-CPNNS 155
Db 205 LNHKV 209
QY 156 VDLKL 160

RESULT 6
ID TNFA_HORSE STANDARD; PRT; 234 AA.
AC P29553;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNFA.
OS EQUUS CABALLUS (HORSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PERISSODACTYLA; EQUIDAE; EQUUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92084125.
RA SU X., MORRIS D.D., MCGRAW R.A.;
RT "Cloning and characterization of gene TNF alpha encoding equine tumor
necrosis factor alpha."
RL GENE 107:319-321(1991).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CACHECTA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
PROTEOLYTIC PROCESSING.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL: M64087; G164245; -
DR PIR: JQ1344; JQ1344.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR PFAM: PF00229; TNF; 1.
DR HSP: P01375; 1TNF.
KW CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
FT PROPEP 1 77 BY SIMILARITY.
FT CHAIN 78 234 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 146 178 BY SIMILARITY.
SQ SEQUENCE 234 AA; 25469 MW; CD20BEE6 CRC32;

Query Match 6.7%; Score 113; DB 1; Length 234;
Best Local Similarity 34.7%; Pred. No. 1.51e-03;
Matches 25; Conservative 16; Mismatches 25; Indels 6; Gaps 6;

Db 83 RTPSDRPVAVH-VANPQAEQQLQWLSGRANALLANGVKLTDLVPLDGLIYSQVLF 141
QY 92 RAPFKKSWAYLQVAKHLNKLKLSW-N-K-DGIL-HGVRYODGNLVIOFPGLYFIICQLQF 147
Db 142 KGGCPSTHVLL 153

FT TRANSMEM 81 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 103 281 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 4 70 PRO-RICH.
 FT DOMAIN 45 65 POLY-PRO.
 FT DISULFID 202 233 BY SIMILARITY.
 FT CARBOHYD 184 184 POTENTIAL.
 FT CARBOHYD 250 250 POTENTIAL.
 FT CARBOHYD 260 260 POTENTIAL.
 SQ SEQUENCE 281 AA; 31485 MW; 714BAA90 CRC32;

Query Match 6.58; Score 111; DB 1; Length 281;
 Best Local Similarity 40.48; Pred. No. 3.09e-03;
 Matches 21; Conservative 7; Mismatches 20; Indels 4; Gaps 3;

Db 160 LEWEDTYGIVLLGKGVKGLVINETGLYFVYKVFYRGSCNNPLSHKV 211
 QY 113 LSNWKG-GI--LHGVRVQDGNLVIFQPLGFIICQLQFLVQ-CPNNSVDLKL 160

RESULT 9
 ID TNFA HUMAN STANDARD; PRT; 233 AA.
 AC P01375;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
 GN TNFA.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87217060.
 RA NEDOSPASOV S.A., SHAKHOV A.N., TURTSKAYA R.L., METT V.A.,
 RA AZIZOV M.M., GEORGIEV G.P., KOBOKO V.G., DOBRYNIN V.N.,
 RA FILIPPOV S.A., BYSTROV N.S., BOLDYREVA E.F., CHUVPILO S.A.,
 RA CHUMAKOV A.M., SHINGAROVA L.N., OVCHINNIKOV Y.A.;
 RT "Tandem arrangement of genes coding for tumor necrosis factor (TNF-
 alpha) and lymphotoxin (TNF-beta) in the human genome.";
 RL COLD SPRING HARB. SYMP. QUANT. BIOL. 51:611-624(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85086244.
 RA PENNICA D., NEDWIN G.E., HAYFLICK J.S., SEEBURG P.H., DERYNCK R.,
 RA PALLADINO M.A., KOHR W.J., AGGARWAL B.B., GOEDDEL D.V.;
 RT "Human tumour necrosis factor: precursor structure, expression and
 homology to lymphotoxin.";
 RL NATURE 312:724-729(1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85137898.
 RA SHIRAI T., YAMAGUCHI H., ITO H., TODD C.W., WALLACE R.B.;
 RT "Cloning and expression in Escherichia coli of the gene for human
 tumour necrosis factor.";
 RL NATURE 313:803-806(1985).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86016093.
 RA JARRETT-NEDWIN J., PENNICA D., GOEDDEL D.V., GRAY P.W.;
 RT "Human lymphotoxin and tumor necrosis factor genes: structure,
 homology and chromosomal localization.";
 RL NUCLEIC ACIDS RES. 13:6361-6373(1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85142190.
 RA WANG A.M., CREASEY A.A., LADNER M.B., LIN L.S., STRICKLER J.,
 RA VAN ARSDELL J.N., YAMAMOTO R., MARK D.F.;
 RT "Molecular cloning of the complementary DNA for human tumor necrosis
 factor.";
 RL SCIENCE 228:149-154(1985).
 RN [6]
 RP SEQUENCE FROM N.A.

RX MEDLINE; 86030296.
 RA MARMENOUT A., FRANSEN L., TAVERNIER J., DER HEYDEN J., TIZARD R.,
 RA KAWASHIMA E., SHAW A., JOHNSON M.J., SEMON D., MUELLER R.,
 RA RUYSSCHAERT M.R., VAN VLIET A., FIERIS W.;
 RT "Molecular cloning and expression of human tumor necrosis factor and
 comparison with mouse tumor necrosis factor.";
 RL EUR. J. BIOCHEM. 152:515-522(1985).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93272029.
 RA IRIS F.J.M., BOUGUELERET L., PRIEUR S., CATERINA D., PRIMAS G.,
 RA PERROT V., JURKA J., RODRIGUEZ-TOME P., CLAVERIE J.-M., DAUSSET J.,
 RA COHEN D.;
 RT "Dense Alu clustering and a potential new member of the NF kappa B
 family within a 90 kilobase HLA class III segment.";
 RL NAT. GENET. 3:137-145(1993).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE; 89159409.
 RA JONES E.Y., STUART D.I., WALKER N.P.;
 RT "Structure of tumour necrosis factor.";
 RL NATURE 338:225-228(1989).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE; 91193276.
 RA JONES E.Y., STUART D.I., WALKER N.P.;
 RT "The structure of tumour necrosis factor -- implications for
 biological function.";
 RL J. CELL SCI. SUPPL. 13:11-18(1990).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE; 90008932.
 RA ECK M.J., SPRANG S.R.;
 RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.
 Implications for receptor binding.";
 RL J. BIOL. CHEM. 264:17595-17605(1989).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT ARG-107.
 RX MEDLINE; 98147459.
 RA REED C., FU Z.O., WU J., XUE Y.N., HARRISON R.W., CHEN M.J.,
 RA WEBER I.T.;
 RT "Crystal structure of TNF-alpha mutant R31D with greater affinity for
 receptor R1 compared with R2.";
 RL PROTEIN ENG. 10:1101-1107(1997).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT M3S.
 RX MEDLINE; 98113178.
 RA CHA S.S., KIM J.S., CHO H.S., SHIN N.K., JEONG W., SHIN H.C.,
 RA KIM Y.J., HAHN J.H., OH B.H.;
 RT "High resolution crystal structure of a human tumor necrosis factor-
 alpha mutant with low systemic toxicity.";
 RL J. BIOL. CHEM. 273:2153-2160(1998).
 RN [13]
 RP MUTAGENESIS.
 RX MEDLINE; 91184128.
 RA OSTADE X.V., TAVERNIER J., PRANCE T., FIERIS W.;
 RT "Localization of the active site of human tumour necrosis factor
 (htnf) by mutational analysis.";
 RL EMBO J. 10:827-836(1991).
 RN [14]
 RP MYRISTOYLATION
 RX MEDLINE; 93018820.
 RA STEVENSON F.T., BURSTEN S.L., LOCKSLEY R.M., LOVETT D.H.;
 RT "Myristyl acylation of the tumor necrosis factor alpha precursor on
 specific lysine residues.";
 RL J. EXP. MED. 176:1053-1062(1992).
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
 CONDITIONS.

GN	TNFA.
OS	PAPIO HAMADRYAS URUSINUS (CHACMA BABOON).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC	PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; PAPIO.
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE; 98147379.
RX	HAUDEK S.B., REDL H., SCHLAG G., GIROIR B.P.;
RT	*Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
RL	alpha.";
EL	MOL. IMMUNOL. 34:1041-1042(1997).
CC	-1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN CONDITIONS.
CC	-1- SUBUNIT: HOMOTRIMER.
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
CC	-1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.
CC	-1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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DR	EMBL; AF019963; G3417555; -.
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PS50049; TNF_2; 1.
KW	CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
FT	PROPEP 1 76 BY SIMILARITY.
FT	CHAIN 77 233 TUMOR NECROSIS FACTOR.
FT	TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT	DISULFID 145 177 BY SIMILARITY.
SQ	SEQUENCE 233 AA; 25658 MW; E38CF6E8 CRC32;
Query Match	6.2%; Score 106; DB 1; Length 233;
Best Local Similarity	39.6%; Pred. No. 1.78e-02;
Matches	19; Conservative 10; Mismatches 17; Indels 2; Gaps 2;
Dd	105 LNRRNALLANGVELDNLVVPSEGLIYVSQVLFKGQGCPNSHVLL 152 : : :: :: :: :: :: :
Oy	113 LSNWKDGIL-HGVRYODGNLVIFPGLYFIQCQLQFLVQ-CPNNVDL 158 : : : :: :: :: :: :
RESULT 13	
ID	FASLRAT STANDARD; PRT; 278 AA.
AC	P36940;
DT	01-JUN-1994 (REL. 29, CREATED)
DT	01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE	FAS ANTIGEN LIAND.
GN	APTLI1GI OR LASL.
OS	RATTUS NORVEGICUS (RAT).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC	RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; RATTUS.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 94084792.
RA	SUDA T., TAKAHASHI T., GOLSTEIN P., NAGATA S.;
RT	"Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family."
RL	CELL 75:1169-1178(1993).

RESULT	15
ID	TNFA_MA
AC	P79337

Search completed: Fri Aug 13 16:42:47 1999
Job time : 14 secs.

WATERMAN

(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:43:05 1999; MasPar time 16.45 Seconds
Tabular output not generated. 776.169 Million cell updates/sec

Title: >US-09-079-785-8
Description: (1-234) from US09079785.pep
Perfect Score: 1697
Sequence: 1 MDPGLQALNGMAPPGDTAM.....DSTFPLENVLSIFLYSNSD 234

Scoring table: PAM 150
Gap 11
Searched: 179066 seqs, 54579741 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: sptrembl9
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertibrate 14:sp.virus
Statistics: Mean 45.009; Variance 85.602; scale 0.526

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1662	97.9	234	4	CD30L PROTEIN.	0.00e+00
2	117	6.9	479	11	PHOSPHOPROTEIN PHOSPHA	2.11e-03
3	117	6.9	499	11	PROTEIN PHOSPHATASE 5.	2.11e-03
4	116	6.8	279	11	FAS LIGAND.	2.95e-03
5	108	6.4	157	4	TUMOR NECROSIS FACTOR	4.08e-02
6	109	6.4	332	10	RIBITOL DEHYDROGENASE	2.96e-02
7	109	6.4	1165	5	SIMILARITY TO PROTEIN-	2.96e-02
8	106	6.2	249	4	TWEAK	7.73e-02
9	101	6.0	225	11	TNF-RELATED WEAK INDUC	3.70e-01
10	102	6.0	240	4	LIGAND FOR HERPESVIRUS	2.72e-01
11	102	6.0	240	4	TUMOR NECROSIS FACTOR	2.72e-01
12	102	6.0	492	13	PROTEIN PHOSPHATASE 5	2.72e-01
13	98	5.8	104	6	TNFA (FRAGMENT).	9.23e-01
14	99	5.8	233	6	TUMOUR NECROSIS FACTOR	6.82e-01
15	98	5.8	233	6	TUMOR NECROSIS FACTOR	9.23e-01
16	98	5.8	619	3	CHROMOSOMAL XV READING	9.23e-01
17	98	5.8	724	10	HYPOTHETICAL 82.5 KD P	9.23e-01
18	99	5.8	1010	5	F55C5.4 PROTEIN.	6.82e-01
19	99	5.8	1684	4	WUGSC-H DJ1186C01.1 PR	6.82e-01
20	96	5.7	216	11	TUMOR NECROSIS FACTOR-	1.68e+00

21	97	5.7	233	11	035734	TUMOR NECROSIS FACTOR	1.25e+00
22	96	5.7	257	1	027054	CONSERVED PROTEIN.	1.68e+00
23	96	5.7	330	3	014133	HYPOTHETICAL 38.0 KD P	1.68e+00
24	95	5.6	228	2	Q55893	TRANSPOSASE.	2.26e+00
25	95	5.6	249	8	Q21289	ATP SYNTHASE A CHAIN (2.26e+00
26	95	5.6	914	10	Q96301	SPINDLY.	2.26e+00
27	95	5.6	914	1	Q39690	DNA POLYMERASE (EC 2.7	2.26e+00
28	95	5.6	1549	4	Q60706	SULFONYLUREA RECEPTOR	2.26e+00
29	95	5.6	1549	4	Q60707	SULFONYLUREA RECEPTOR	2.26e+00
30	93	5.5	207	5	Q17097	F40H7.1 PROTEIN.	4.06e+00
31	94	5.5	281	2	P11594	HYPOTHETICAL 30.3 KD P	3.03e+00
32	93	5.5	420	2	Q30677	GYRASE BETA SUBUNIT (F	4.08e+00
33	94	5.5	437	14	Q41953	KINASE.	3.03e+00
34	94	5.5	541	5	Q20214	F40F12.4 PROTEIN.	3.03e+00
35	94	5.5	569	6	Q28616	ANTI-MULLERIAN HORMONE	3.03e+00
36	93	5.5	717	14	Q65156	PC717R.	4.06e+00
37	94	5.5	1066	5	Q18902	CODED FOR BY C. ELEGAN	3.03e+00
38	94	5.5	1335	14	Q89353	ASN/THR/SER/ILE RICH P	3.03e+00
39	93	5.5	1545	11	Q89115	SULFONYLUREA RECEPTOR	4.06e+00
40	93	5.5	1545	11	Q63563	SULFONYLUREA RECEPTOR.	4.06e+00
41	92	5.4	156	11	Q62326	TUMOR NECROSIS FACTOR.	5.42e+00
42	92	5.4	232	11	Q35853	TUMOR NECROSIS FACTOR	5.42e+00
43	92	5.4	282	5	Q02201	HYPOTHETICAL 32.4 KD P	5.42e+00
44	92	5.4	364	5	P91384	COSMID K12D9.	5.42e+00
45	92	5.4	1283	4	Q43933	PEROXISOME BIOGENESIS	5.42e+00

ALIGNMENTS

RESULT 1
ID O43404 PRELIMINARY; PRT; 234 AA.
AC O43404:
DT 01-JUN-1998 (TREMUREL. 06, CREATED)
DT 01-JUN-1998 (TREMUREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMUREL. 08, LAST ANNOTATION UPDATE)
DE CD30L PROTEIN.
GN CD30L.
OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98007874.
RA CROAGER E.J., ABRAHAM L.J.;
RT "Characterisation of the human CD30 ligand gene structure.";
RL BIOCHIM. BIOPHYS. ACTA 1353:231-235(1997).
DR EMBL; AF006384; G2815515;
DR EMBL; AF006381; G2815515; JOINED.
DR EMBL; AF006382; G2815515; JOINED.
DR EMBL; AF006383; G2815515; JOINED.
DR PROSITE; PS00251; TNF_L1;
SQ SEQUENCE 234 AA; 25963 MW; B6137845 CRC32;

Query Match	97.9%;	Score 1662;	DB 4;	Length 234;
Best Local Similarity	98.3%;	Pred. No. 0.00e+00;		
Matches	230;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
Db	1	MDPGLQALNGMAPPGDTAMHVPAGSVASHLGTTSRYSFYLTATLALCLVFTATIMVL	60	
Qy	1	MDPGLQALNGMAPPGDTAMHVPAGSVASHLGTTSRYSFYLTATLALCLVFTATIMVL	60	
Db	61	VVQRTDSIPNSPDNVPKGGNCSEDLICILRAPFKKSWAYLOVAKHLNKTLSWNKDG1	120	
Qy	61	VVQRTDSIPNSPDNVPKGGNCSEDLICILRAPFKKSWAYLOVAKHLNKTLSWNKDG1	120	
Db	121	LHGVRQDGNLVIOPGYFIICQLQFLVQCPNNSVDLKKXELLINKHKXOLVTVCESS	180	
Qy	121	LHGVRQDGNLVIOPGYFIICQLQFLVQCPNNSVDLKKXELLINKHKXOLVTVCESS	180	
Db	181	MQTKHVQNLQFLDLYQVNTTISVNVDTQYIDTSTFFPLENVLSIFLYSNSD	234	
Qy	181	MQTKHVQNLQFLDLYQVNTTISVNVDTQYIDTSTFFPLENVLSIFLYSNSD	234	

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AC Q61217;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FAS LIGAND.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
CC SCIURIFORMES; MORIDAE; MORINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA FENNER M.H., SHIODA T., ISSELBACHER K.J.;
RL SUBMITTED (MAY-1996) TO EMBL/GENEBANK/DBJ DATA BANKS.
DR EMBL: U58995; G1389772; -.
DR PROSITE; PS00251; TNF_1; 1.
DR PFAM: PF00229; TNF; 1.
SQ SEQUENCE 279 AA; 31340 MW; 9062DF08 CRC32;

Query Match          6.8%; Score 116; DB 11; Length 279;
Best Local Similarity 35.4%; Pred. No. 2.95e-03;
Matches 23; Conservative 9; Mismatches 29; Indels 4; Gaps 4;

Db 145 AHLGNPHRSRISPLEWEDTGTALISGVKKYKKGGLVINEAGLVFYVKVYFGSGCNQP 204
Qy 100 AYLOVAHLNKTLSWNKD-GI-L-HGVR YODGNLVIOFPGLYFIICQLQFLVO-CPNNS 155
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 205 LNHKV 209
Qy 156 VDLKL 160
| |
RESULT 5
ID ID 043647 PRELIMINARY; PRT; 157 AA.
AC AC 043647;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE DE TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).
GN TNFA.
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC JANG J.S., KIM B.E.;
RL SUBMITTED (JAN-1998) TO EMBL/GENEBANK/DBJ DATA BANKS.
DR EMBL: AF043342; G2905634; -.
DR PROSITE; PS00251; TNF_1; 1.
FT NON_TER _1
SQ SEQUENCE 157 AA; 17380 MW; FD78F0A6 CRC32;

Query Match          6.4%; Score 108; DB 4; Length 157;
Best Local Similarity 36.1%; Pred. No. 4.08e-02;
Matches 26; Conservative 14; Mismatches 26; Indels 6; Gaps 5;

Db 6 RTPSKDPVAHV-VANPOAQEQQLWLNRRALLANGVELRDNLVVPSEGLYLIYSQVLV 64
Qy 92 RAPFKSWAYLQVAKHLNKTLSW-NK--DGIL-HGVR YODGNLVIOFPGLYFIICQLQF 147
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 65 KGQCPCPTHVLL 76
Qy 148 LVQ-CPNNSVDL 158
| | | | |

RESULT 6
ID ID 022985 PRELIMINARY; PRT; 332 AA.
AC AC 022985;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE REBIOTOL DEHYDROGENASE ISOLOG.
GN TI9F06.14.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

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Query Match 6.0%; Score 101; DB 11; Length 225;
Best Local Similarity 38.5%; Pred. No. 3.70e-01;
Matches 15; Conservative 13; Mismatches 8; Indels

Db 125 QIGFTVIRAGLYLYQVHF--D-EGKAVYLKLLVN 160
 QY 127 QDGNLVIOFPGLYFIQQLVOCNNSVDLKLLELIN 165

RESULT 10
 ID O75476 PRELIMINARY; PRT; 240 AA.
 AC O75476
 DT 01-NOV-1998 (TREMELREL. 08, CREATED)
 DT 01-NOV-1998 (TREMELREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE LIGAND FOR HERPESVIRUS ENTRY MEDIATOR.
 GN HVEM-L.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HARROP J.A., McDONNELL P.C., BRIGHAM-BURKE M., LYN S.D., MINTON J.,
 RA TAN K.B., DEDE K., SPAMPANATO J., SILVERMAN C., HENSLEY P.,
 RA DIPRINIO R., EMERY J.G., DEEN K., EICHMAN C., CHABOT-FLETCHER M.,
 RA TRONER A., YOUNG P.R.;
 RT "HVEM-L, a novel ligand for HVEM/TR2, stimulates NF-kB-dependent
 RT transcription, proliferation of T cells and inhibition of HT29 cell
 RT growth."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA SHINTANI Y., NISHI K., LYNN S.D., YOUNG P.R.;
 RL SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF064090; G3283356; -
 SQ SEQUENCE 240 AA; 26350 MW; 3490EB77 CRC32;

Query Match 6.0%; Score 102; DB 4; Length 240;
 Best Local Similarity 40.0%; Pred. No. 2.72e-01;
 Matches 14; Conservative 10; Mismatches 10; Indels 1; Gaps 1;
 Db 121 AFLGLSYHDGALVTKAGYVYIYKVLGGVCCP 155
 QY 119 GILHGVYDGNLVIOFPGLYFIQQLVOCPL 152

RESULT 11
 ID O43557 PRELIMINARY; PRT; 240 AA.
 AC O43557
 DT 01-JUN-1998 (TREMELREL. 06, CREATED)
 DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMELREL. 06, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR SUPERFAMILY MEMBER LIGHT.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MAURI D.N., EBER R., MONTGOMERY R.I., KOCHER K.D., CHEUNG T.C.,
 RA YU G.-L., RUBEN S., MURPHY M., EISENBERG R.J., COHEN G.H., SPEAR P.G.,
 RA WARE C.F.;
 RL IMMUNITY 8:21-30(1998).
 DR EMBL: AF036581; G2815624; -
 SQ SEQUENCE 240 AA; 26351 MW; 4A4B603A CRC32;

Query Match 6.0%; Score 102; DB 4; Length 240;
 Best Local Similarity 40.0%; Pred. No. 2.72e-01;
 Matches 14; Conservative 10; Mismatches 10; Indels 1; Gaps 1;
 Db 121 AFLGLSYHDGALVTKAGYVYIYKVLGGVCCP 155
 QY 119 GILHGVYDGNLVIOFPGLYFIQQLVOCPL 152

RESULT 12
 ID O42205 PRELIMINARY; PRT; 492 AA.
 AC O42205
 DT 01-JAN-1998 (TREMELREL. 05, CREATED)
 DT 01-JAN-1998 (TREMELREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE PROTEIN PHOSPHATASE 5 (FRAGMENT).
 GN PP5.
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
 OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA OLLENDORFF V., DONOGHUE D.J.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF018263; G2407639; -
 DR PFAM: PF00149; STphosphatase; 1.
 DR PFAM: PF00515; TPR; 2;
 FT NON_TER 1
 SQ SEQUENCE 492 AA; 56144 MW; C503341E CRC32;

AC O42205;
 DT 01-JAN-1998 (TREMELREL. 05, CREATED)
 DT 01-JAN-1998 (TREMELREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE PROTEIN PHOSPHATASE 5 (FRAGMENT).
 GN PP5.
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
 OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA OLLENDORFF V., DONOGHUE D.J.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF018263; G2407639; -
 DR PFAM: PF00149; STphosphatase; 1.
 DR PFAM: PF00515; TPR; 2;
 FT NON_TER 1
 SQ SEQUENCE 492 AA; 56144 MW; C503341E CRC32;

Query Match 6.0%; Score 102; DB 13; Length 492;
 Best Local Similarity 23.9%; Pred. No. 2.72e-01;
 Matches 21; Conservative 28; Mismatches 33; Indels 6; Gaps 6;
 Db 201 CLYQMLVQV-KDLS-KLPSLVEVSLEKSOQVTVVC-GDTHG-QFYDLNIFHLNGLPSEN 256
 QY 143 CQLQFLVQCPNNSVDLKLLEINKHKKQALVTVCESGMOTKHVYQNLSQLLDYLVQNT 202

Db 257 NPYI-FNG-DFVDRGSGFSVEVITLFGF 282
 QY 203 TISVNVDTFOYIDTFTFPLENLSIFLY 230

RESULT 13
 ID Q27978 PRELIMINARY; PRT; 104 AA.
 AC Q27978
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE TNEA (FRAGMENT).
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE; BOS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HOLSTEIN;
 RA DIETZ A.B., NEIBERGS H.L., KEHLI M.E.;
 RL SUBMITTED (JUN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U11040; G507912; -
 DR PROSITE: PS00251; TNF_1; 1.
 DR PFAM: PF00229; TNF; 1.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11662 MW; 29A2EC93 CRC32;

Query Match 5.8%; Score 98; DB 6; Length 104;
 Best Local Similarity 38.9%; Pred. No. 9.23e-01;
 Matches 14; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
 Db 26 NGVKLEDNOLVWPADGLYLIYSQVLFGRGCGCPSTPL 61
 QY 122 HGVRYDGNLVIOFPGLYFIQQLVOCPL 156

RESULT 14
 ID O77764 PRELIMINARY; PRT; 233 AA.
 AC O77764
 DT 01-NOV-1998 (TREMELREL. 08, CREATED)
 DT 01-NOV-1998 (TREMELREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE TUMOUR NECROSIS FACTOR ALPHA.
 GN TNF.
 OS MACROPUS EUGENII (TAMMAR WALLABY).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; METATHERIA;

W P S R E A

(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Aug 13 16:45:57 1999; MasPar time 10.27 Seconds
Tabular output not generated. 455.481 Million cell updates/sec

Title: >US-09-079-785-19
Description: (1-220) from US09079785.pep
Perfect Score: 1588
Sequence: 1 MQVQPGSVASPRWTRPWS.....DTNTPDLNLSVFLYSSSD 220

Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1: part1 2: part2 3: part3 4: part4 5: part5 6: part6 7: part7
8: part8 9: part9 10: part10 11: part11 12: part12 13: part13
14: part14 15: part15 16: part16 17: part17 18: part18
19: part19 20: part20 21: part21 22: part22 23: part23
24: part24 25: part25 26: part26 27: part27 28: part28
29: part29 30: part30 31: part31 32: part32 33: part33
34: part34 35: part35 36: part36 37: part37 38: part38
39: part39

Statistics: Mean 32.401; Variance 152.561; scale 0.212

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1588	100.0	220	8 R45006	Sequence encoded by a	7.48e-130
2	1588	100.0	239	8 R45008	Sequence encoded by a	7.48e-130
3	1189	74.9	215	8 R45007	Sequence encoded by a	8.71e-94
4	1189	74.9	234	8 R45009	Sequence encoded by a	8.71e-94
5	113	7.1	137	14 R79087	Mouse Fas ligand (par	1.91e+00
6	113	7.1	138	14 R79088	Mouse Fas ligand (par	1.91e+00
7	113	7.1	179	14 R79085	Mouse Fas ligand (par	1.91e+00
8	113	7.1	279	18 R88357	Mouse Fas ligand.	1.91e+00
9	113	7.1	279	14 R79098	Mouse Fas ligand.	1.91e+00
10	113	7.1	279	14 R77282	Mouse Fas-l protein.	1.91e+00
11	107	6.7	397	2 R70261	Sequence of rat glia	5.04e+00
12	101	6.4	137	14 R79085	Rat Fas ligand (parti	1.31e+01
13	101	6.4	138	14 R79085	Rat Fas ligand (parti	1.31e+01
14	101	6.4	179	14 R79066	Rat Fas ligand (parti	1.31e+01
15	101	6.4	278	14 R79095	Rat Fas ligand encode	1.31e+01
16	100	6.3	189	34 W29746	TNF related endotheli	1.53e+01

17	100	6.3	249	34	W29745	TNF related endotheli	1.53e+01
18	100	6.3	284	30	W47525	Homo sapiens tumour n	1.53e+01
19	98	6.2	149	2	R03264	Tumorigenic polyepiti	2.09e+01
20	98	6.2	180	23	W10875	Fast/Lt-alpha hybrid.	2.09e+01
21	99	6.2	690	37	W77414	Human sodium dependen	1.79e+01
22	95	6.0	374	32	W36994	Human secreted protei	3.33e+01
23	94	5.9	130	14	R79096	Human Fas ligand C-te	3.88e+01
24	94	5.9	136	14	R88307	N-terminally deleted	3.88e+01
25	94	5.9	137	14	R88306	N-terminally deleted	3.88e+01
26	94	5.9	138	14	R79064	Human Fas ligand (par	3.88e+01
27	94	5.9	138	14	R88305	N-terminally deleted	3.88e+01
28	94	5.9	139	14	R88304	N-terminally deleted	3.88e+01
29	94	5.9	141	14	R88303	N-terminally deleted	3.88e+01
30	94	5.9	145	27	W35848	Human FAS-ligand for	3.88e+01
31	94	5.9	151	26	W16667	Human Fas ligand (hfa	3.88e+01
32	94	5.9	178	14	R88308	C-terminally deleted	3.88e+01
33	94	5.9	265	33	W48954	Non-cleavable Fas lig	3.88e+01
34	94	5.9	268	33	W48953	Non-cleavable Fas lig	3.88e+01
35	94	5.9	281	14	R77281	Human Fas-L protein.	3.88e+01
36	94	5.9	281	26	W27143	Human Fas ligand.	3.88e+01
37	94	5.9	281	35	W49105	Human Fas ligand.	3.88e+01
38	94	5.9	281	36	W75959	Human Fas ligand.	3.88e+01
39	94	5.9	281	18	R88104	Human Fas ligand.	3.88e+01
40	94	5.9	281	18	R88356	CH3/Fas Ligand domain	3.88e+01
41	94	5.9	287	26	W27146	Human FAS-ligand:lgG2	3.88e+01
42	94	5.9	378	27	W35864	Human FAS-ligand:lgG2	3.88e+01
43	94	5.9	397	4	R20089	PN-I alpha analogue,	3.88e+01
44	94	5.9	397	4	R20086	Sequence of protease	3.88e+01
45	94	5.9	397	4	R20086	PN-I alpha analogue,	3.88e+01

ALIGNMENTS

RESULT 1
ID R45006 standard; Protein; 220 AA.
AC R45006;
DE 19-JUN-1994 (first entry)
DT Sequence encoded by a murine CD30-L cDNA clone.
DE Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
OS Acomys cahirinus.
FT Key Location/Qualifiers
FT region 28..48
FT /label- transmembrane
PN W09324135-A.
PD 09-DEC-1993.
PR 25-MAY-1993; U04926.
PR 26-MAY-1992; US-889717.
PR 02-JUN-1992; US-892459.
PR 15-JUN-1992; US-895660.
PR 01-JUL-1992; US-907224.
PR 27-OCT-1992; US-966775.
PA (IMMV) IMMUNEX CORP.
PI Armitage RJ, Goodwin RG, Smith CA;
DR WPI: 93-405417/50.
DR N-PSDB; Q53535.
PT New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
PS Claim 15; Figure 3a; 59pp; English.
CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prepd from
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
CC This cDNA can then be used as a probe to screen a human PBL cDNA
CC library to obtain cDNA encoding human CD30-L.
SQ Sequence 220 AA;

Query Match 100.0%; Score 1588; DB 8; Length 220;

Best Local Similarity 100.0%; Pred. No. 7.48e-130;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mqvqgsvaspwrtspwrtstsrsvfylstaltclvavaiilvlvqgkdstpnttek 60
QY 1 MQVQGSVASPWRSTPWRSTSRSVFYLTALTCLVAVAILVLVQVKDSTPNTTEK 60

Db 61 aplkgncsedlftclktstpskswaylqvskhlnntklswnedgtihgliyqdgnlivq 120
QY 61 APLKGNCSDELFTCLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTHGLIYQDGNLIQV 120

Db 121 fpolyfivcoqlfivcshsvedltlqlinsikkktlvtvcesgvqskniyqnlisqfl 180
QY 121 FPOLYFIVCOQLFIVCSHNSVDLTQLQLINSIKKQTLVTVCESGVSKNIYQNLISQFL 180

Db 181 lhylqvntisvrdnfvqyvdnttflpdnvlsvflysssd 220
QY 181 LHYLQVNTISVRDNFQYVDNTTFPLDNVLSVFLYSSSD 220

RESULT 2
ID R45008 standard; Protein: 239 AA.
AC R45008;
DT 19-JUN-1994 (first entry)
DE Sequence encoded by a murine CD30-L cDNA clone
KW encoding additional N-terminal amino acids.
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
OS Acomys cahirinus.
FH Key Location/Qualifiers
FT region 47..67
FT /label= Transmembrane
FT W09324135-A.
PN 09-DEC-1993.
PD 25-MAY-1993; U04926.
PE 26-MAY-1992; US-889717.
PR 02-JUN-1992; US-892459.
PR 15-JUN-1992; US-899660.
PR 01-JUL-1992; US-907224.
PR 27-OCT-1992; US-966775.
PA (IMV) IMMUNEX CORP.
PI Armitage RJ, Goodwin RG, Smith CA;
DR MPI; 93-405417/50.
DR N-PSDB; Q53537.
PT New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
PT
PS Claim 15; Figure 6a; 59pp; English.
CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prep. from
CC the murine helper T-cell line 789 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC (Q53535). This cDNA can then be used as a probe to screen a human PBL
CC cDNA library to obtain cDNA encoding human CD30-L (Q53536). An anchored
CC PCR technique was employed to isolate CD30-L human and murine clones
CC containing an additional 19 N-terminal amino acid sequence (Q53537,
CC Q53538).
SQ Sequence 239 AA;

Query Match 100.0%; Score 1588; DB 8; Length 239;
Best Local Similarity 100.0%; Pred. No. 7.48e-130;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 mqvqgsvaspwrtspwrtstsrsvfylstaltclvavaiilvlvqgkdstpnttek 79
QY 1 MQVQGSVASPWRSTPWRSTSRSVFYLTALTCLVAVAILVLVQVKDSTPNTTEK 60

Db 80 aplkgncsedlftclktstpskswaylqvskhlnntklswnedgtihgliyqdgnlivq 139
QY 80 APLKGNCSDELFTCLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTHGLIYQDGNLIQV 139

CC The expressed protein can be used to suppress and prevent

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Db 145 ahltnphrsrslpewdytgaltisgvykkgglvinetgltfyvskvyfrgscnnqp 204
 QY 86 AYLVQSKHLNNTKLSWNED-GT--IHGLIYQDGNLIVQFGLYFIVCQLQFLVQ-CSNHS 141

Db 205 ln 206
 QY 142 VD 143

RESULT 10

ID R77282 standard; Protein; 279 AA.
 AC R77282;
 DE Mouse Fas-L protein.
 KW Fas ligand; Fas-L; cell surface protein; autoimmune disease;
 KW self-tolerance.
 OS Mus sp.

FH Key Location/Qualifiers
 FT domain 1..78
 FT domain /label= Cytoplasmic_domain
 FT domain 79..103
 FT domain /label= Transmembrane_domain
 FT domain 104..279
 FT domain /label= Extracellular_domain

PN WO9518819-A.
 PD 13-JUL-1995.
 PF 06-JAN-1995; U00362.
 PR 07-JAN-1994; US-179138.
 PR 01-FEB-1994; US-190559.
 PA (IMV) IMMUNEX CORP.
 PI Goodwin RG.
 DR WPI: 95-255032/33.
 DR N-PSDB; Q91312.

PT Human and murine DNA encoding ligand(s) binding to cell surface protein
 PT Fas - useful for studying auto-immune disorder(s) and development of
 PT self-tolerance.
 PS Disclosure; Page 29-30; 38pp; English.
 CC A cDNA library prepd. from mouse peripheral blood lymphocyte mRNA was
 CC screened with a murine Fas-L probe from the 3' end of Fas-L DNA.
 CC An isolated clone (Q91312) encoded mouse Fas-L.
 SQ Sequence 279 AA;

Query Match 7.1%; Score 113; DB 14; Length 279;
 Best Local Similarity 32.3%; Pred. No. 1.91e+00;
 Matches 20; Conservative 14; Mismatches 24; Indels 4; Gaps 3;

Db 145 ahltnphrsrslpewdytgaltisgvykkgglvinetgltfyvskvyfrgscnnqp 204
 QY 86 AYLVQSKHLNNTKLSWNED-GT--IHGLIYQDGNLIVQFGLYFIVCQLQFLVQ-CSNHS 141

Db 205 ln 206
 QY 142 VD 143

RESULT 11

ID P70261 standard; Protein; 397 AA.
 AC P70261;
 DT 29-MAY-1991 (first entry)
 DE Sequence of rat glia-derived neurite-promoting factor (GdnPF).
 KW Nerve fibre regeneration; neurite promoter;
 KW serine protease inhibitor.
 OS Rat.

FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Peptide /note= "may be omitted"
 FT protein 20..397

PN Ep-233838-A.
 PD 26-AUG-1987.
 PF 29-JAN-1987; 810057.
 PR 04-FEB-1986; GB-002626.
 PR 11-FEB-1986; GB-003334.
 PR 31-JUL-1986; GB-018760.

PA (CIBA) CIBA GEIGY AG.
 PI Monard D, Odink KG, Gloor S;
 DR WPI: 87-236863/34.
 DR N-PSDB; N70395.
 PT Recombinant human glia derived neurite-promoting factor - used
 PT for promoting nerve fibre regeneration following lesions in the
 PT nervous system
 PS Disclosure; pp26-28; 36pp; English.
 CC For the prepn. of human GdnPF, the cDNA library is pref. derived
 CC from human glioma cells, eg from the human glioma cell line LN340.
 CC For the prepn. of related peptides, eg rat GdnPF, other glial cells,
 CC eg C6 rat glioma cells, are used to prepare a cDNA library. The
 CC neurite-promoting and serine protease-inhibiting properties of
 CC GdnPF, related peptides and fragments make them useful for promoting
 CC nerve fibre regeneration following lesions in the nervous system,
 CC and for interfering with the migration of normal and tumour cells.
 SQ Sequence 397 AA;

Query Match 6.7%; Score 107; DB 2; Length 397;
 Best Local Similarity 30.1%; Pred. No. 5.04e+00;
 Matches 31; Conservative 26; Mismatches 41; Indels 5; Gaps 5;

Db 285 vpkrmqlvlpkftalagtdlkeplkalgite-ifepskanfakitrshylqkak 343
 QY 40 VAILVLVQKDKSTPNTTERAPLKGNCSEDLFTLSTPSKKSWA-YLVQSKHLNNTK 98

Db 344 levsedgtkaavv-ttalliarssppwfv-drpflf-cirhn 383
 QY 99 LSWNEDGTHGLIYQDGNLIVQFGLYFIVCQLQFLVQCSNHS 141

RESULT 12

ID R79065 standard; Protein; 137 AA.
 AC R79065;
 DT 22-FEB-1996 (first entry)
 DE Rat Fas ligand (partial sequence).
 KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
 KW Fas cell surface antigen; Fas-L; rat.
 OS Rattus rattus.
 PN WO9513293-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; J01899.
 PR 10-NOV-1993; JP-305975.
 PR 13-DEC-1993; JP-342526.
 PR 18-MAR-1994; JP-074344.
 PR 08-JUL-1994; JP-180955.
 PR 07-SEP-1994; JP-239363.
 PR 18-OCT-1994; JP-278378.
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PA (OSAB-) OSAKA BIOSCIENCE INST.
 PI Nagata S, Nakamura N, Suda T, Takahashi T;
 DR WPI: 95-194031/25.
 DR N-PSDB; Q99494.

PT Peptide which binds to Fas antigen, and antibody reactive with it
 PT for treatment and diagnosis of viral or auto-immune diseases
 PS Claim 5; Page 212-213; 300pp; Japanese.
 CC Fas ligands or active fragments able to induce apoptosis in cells
 CC which express the Fas cell surface antigen are claimed. The
 CC proteins are isolated from human, rat and mouse sources. The present
 CC sequence represents part of the rat Fas ligand.
 SQ Sequence 137 AA;

Query Match 6.4%; Score 101; DB 14; Length 137;
 Best Local Similarity 33.3%; Pred. No. 1.31e+01;
 Matches 16; Conservative 13; Mismatches 15; Indels 4; Gaps 3;

Db 16 lewdtygtalisgvykkgglvineaglyfvykvyfrgscnnqp 63
 QY 99 LSWNED-GT--IHGLIYQDGNLIVQFGLYFIVCQLQFLVQ-CSNHS 142

RESULT 13

ID R79063 standard; Protein; 138 AA.

```

Db      58 lewedtygtalisgvykkgglvineaglyfvyskyfvgqscnsqpl 105
|::|| | || | :: :||||: | | |:|:::
Qy     99 LSNWED-GT--IHGLIYDGNLIIVQFPGFLFYICVLQLVQC-CSNSHV 142

RESULT    15
ID R79095 standard; Protein; 278 AA..
AC R79095;
DE 20-FEB-1996 (first entry)
DT Rat Fas ligand encoded by cDNA clone PTN24-15.
KW Ras ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; rat; Fas-L.
OS Rattus rattus.
FH Key
FT Location/Qualifiers
   FT 77...99
   FT /label= transmembrane_anchor
   FT modified_site 116
   FT /label= N-glycosylation_site
   FT modified_site 130
   FT /label= N-glycosylation_site
   FT modified_site 247
   FT /label= N-glycosylation_site
   FT modified_site 257
   FT /label= N-glycosylation_site
   PN WO9513293-A1.
   PD 18-MAY-1995.
   PF 10-NOV-1994; J01899
   PR 10-NOV-1993; JP-305975.
   PR 13-DEC-1993; JP-342526.
   PR 18-MAR-1994; JP-074344.
   PR 08-JUL-1994; JP-180955.
   PR 07-SEP-1994; JP-239363.
   PR 18-OCT-1994; JP-278378.
   PA (MOCH ) MOCHIDA PHARM CO LTD.
   PP (OSAB-) OSAKA BIOSCIENCE INST.
   PI Nagata S , Nakamura N , Suda T , Takahashi T ;
   DI WPI: 95-194031/25.
   DR N-PDSB; Q94153 , T03656.
PE Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto-immune diseases
PS Claim 8; Fig 2 and 3; 300pp; Japanese.
CC Clones contg. rat cDNA fragments that encoded Fas ligand-like
CC proteins were identified by antibody panning. Clone pTN24-15 was
CC isolated and sequenced (Q94153). The sequence includes an open
CC reading frame coding for a predicted amino acid sequence of
CC 278 residues. The deduced protein sequence (R79095) contains a
CC transmembrane anchor region and 4 consensus N-glycosylation sites
CC the protein is claimed Fas ligand able to induce apoptosis in
CC cells which express the Fas cell surface antigen.
SQ Sequence 278 AA;

Query Match          6.4%; Score 101; DB 14; Length 278;
Best Local Similarity 33.3%; Pred. No. 1,3le+01;
Matches 16; Conservative 13; Mismatches 15; Indels 4; Gaps 0

Db      157 lewedtygtalisgvykkgglvineaglyfvyskyfvgqscnsqpl 204
|::|| | || | :: :||||: | | |:|:::
Qy     99 LSNWED-GT--IHGLIYDGNLIIVQFPGFLFYICVLQLVQC-CSNSHV 142

Search completed: Fri Aug 13 16:46:42 1999
Job time : 45 secs.
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CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REFERENCE/DOCKET NUMBER: 32,172
CC REGISTRATION NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 19:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 220 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 220 AA; 24724 MW; 283693 CN;
SQ
Query Match 100.0%; Score 1588; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 6,70e-130;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MOVQPGSVASPRSTRPWRSTRSRYFYLSTALVCLVAVAILLVVQVKDSTPNTTEK 60
QY 1 MOVQPGSVASPRSTRPWRSTRSRYFYLSTALVCLVAVAILLVVQVKDSTPNTTEK 60
Db 61 APLKGGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLSWNEGTTHGLIYQDGNLIQ 120
QY 61 APLKGGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLSWNEGTTHGLIYQDGNLIQ 120
Db 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCESGVQSKNIYQNLQSOFL 180
QY 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCESGVQSKNIYQNLQSOFL 180
Db 181 LHYLQVNSTISVRVDFQYVDTNFTPLDNVLSVFLYSSSD 220
QY 181 LHYLQVNSTISVRVDFQYVDTNFTPLDNVLSVFLYSSSD 220
RESULT 2
ID US-08-580-014-19 STANDARD; PRT: 220 AA.
XX
AC xxxxxx
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DT
XX
XX
DE Sequence 19, Application US/08580014
XX
XX
CC Sequence 19, Application US/08580014
CC Patent No. 5753203
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5753203el Cytokine That Blinds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/580,014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 19:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 220 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 220 AA; 24724 MW; 283693 CN;
SQ
Query Match 100.0%; Score 1588; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 6,70e-130;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MOVQPGSVASPRSTRPWRSTRSRYFYLSTALVCLVAVAILLVVQVKDSTPNTTEK 60
QY 1 MOVQPGSVASPRSTRPWRSTRSRYFYLSTALVCLVAVAILLVVQVKDSTPNTTEK 60
Db 61 APLKGGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLSWNEGTTHGLIYQDGNLIQ 120
QY 61 APLKGGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLSWNEGTTHGLIYQDGNLIQ 120
Db 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCESGVQSKNIYQNLQSOFL 180
QY 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCESGVQSKNIYQNLQSOFL 180
Db 181 LHYLQVNSTISVRVDFQYVDTNFTPLDNVLSVFLYSSSD 220
QY 181 LHYLQVNSTISVRVDFQYVDTNFTPLDNVLSVFLYSSSD 220
RESULT 3
ID US-08-225-989-19 STANDARD; PRT: 220 AA.
XX
AC xxxxxx
XX
DT
XX
XX
DE Sequence 19, Application US/08225989
XX
XX
CC Sequence 19, Application US/08225989
CC Patent No. 5480981
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.

CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 19:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 220 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 220 AA; 24724 MW; 283693 CN;
Query Match 100.0%; Score 1588; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 6.70e-130;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MQVQPGSVASPRSTRPWRSTRSRYSFYLSLTALVCLVAVAILLVVQVKDSTPNTTEK 60
QY 1 MQVQPGSVASPRSTRPWRSTRSRYSFYLSLTALVCLVAVAILLVVQVKDSTPNTTEK 60
Db 61 APLKGGNCSEDLCTKSTPSKSWAYLOYSKHLNNTKLSWNEDGTHGLYQDGNLIQ 120
QY 61 APLKGGNCSEDLCTKSTPSKSWAYLOYSKHLNNTKLSWNEDGTHGLYQDGNLIQ 120
Db 121 FPGLYFVFCQLQFLVQCNSHSDVLTQLLNSKIKKOTLVTVCSGVQSKNIYQNLQSOFL 180
QY 121 FPGLYFVFCQLQFLVQCNSHSDVLTQLLNSKIKKOTLVTVCSGVQSKNIYQNLQSOFL 180
Db 181 LHYLQVNSTISVRVDNQYVDNTFFPLDNLVSLVFLYSSSD 220
QY 181 LHYLQVNSTISVRVDNQYVDNTFFPLDNLVSLVFLYSSSD 220

RESULT 4

ID US-08-570-923-6 STANDARD; PRT; 239 AA.
XX xxxxxx
XX
DT
XX Sequence 6, Application US/08570923
DE Patent No. 5677430
XX GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 239 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 239 AA; 26519 MW; 334382 CN;
Query Match 100.0%; Score 1588; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 6.70e-130;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 20 MQVQPGSVASPRSTRPWRSTRSRYSFYLSLTALVCLVAVAILLVVQVKDSTPNTTEK 79
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QY 1 MOVQPGSVASPRSTRPWRSTSRYSFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60
CC
CC
DB 80 APLKGGNCSEDLFTLKSTPSKSWAYLOVSKHLNNTKLSWNEGTIHLIYQDGNLIQ 139
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QY 61 APLKGGNCSEDLFTLKSTPSKSWAYLOVSKHLNNTKLSWNEGTIHLIYQDGNLIQ 120
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CC
QY 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCEGVSQSKNIYQNLQSOFL 180
CC
DB 200 LHYLVQNSTISVRDNFQYVDNTFTPLDNVLSVFLYSSD 239
CC
QY 181 LHYLVQNSTISVRDNFQYVDNTFTPLDNVLSVFLYSSD 220
CC
RESULT 5
ID US-08-580-014-6 STANDARD; PRT; 239 AA.
XX
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DE Sequence 6, Application US/08580014
CC
CC Sequence 6, Application US/08580014
CC Patent No. 5753203
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580.014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225.989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966.775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 239 AA; 26519 MW; 334382 CN;
Query Match 100.0%; Score 1588; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 6.70e-130;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 20 MOVQPGSVASPRSTRPWRSTSRYSFYLTALVCLVAVAILLVVQKKDSTPNTTEK 79
QY 1 MOVQPGSVASPRSTRPWRSTSRYSFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60
DB 80 APLKGGNCSEDLFTLKSTPSKSWAYLOVSKHLNNTKLSWNEGTIHLIYQDGNLIQ 139
QY 61 APLKGGNCSEDLFTLKSTPSKSWAYLOVSKHLNNTKLSWNEGTIHLIYQDGNLIQ 120
DB 140 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCEGVSQSKNIYQNLQSOFL 199
QY 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCEGVSQSKNIYQNLQSOFL 180
DB 200 LHYLVQNSTISVRDNFQYVDNTFTPLDNVLSVFLYSSD 239
QY 181 LHYLVQNSTISVRDNFQYVDNTFTPLDNVLSVFLYSSD 220
RESULT 6
ID US-08-225-989-6 STANDARD; PRT; 239 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 6, Application US/08225989
CC
CC Sequence 6, Application US/08225989
CC Patent No. 5480981
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225.989
CC FILING DATE: 12 APRIL 1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:

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CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 239 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 239 AA; 26519 MW; 334382 CN;

Query Match 100.0%; Score 1588; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 6.70e-130;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 MQVQPSVASPWRSTRPWRSTRSYFVLTALVCLVAVAILVLVVKQKSDTPNTEK 79
QY 1 MQVQPSVASPWRSTRPWRSTRSYFVLTALVCLVAVAILVLVVKQKSDTPNTEK 60

Db 80 APLKGGNCSEDLCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 139
QY 61 APLKGGNCSEDLCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120

Db 140 FPGLYFVFCQFLVQCSNHSVDLTQLLNSKIKKQTLVTVCEGVSQSKNIYQNLISOFL 199
QY 121 FPGLYFVFCQFLVQCSNHSVDLTQLLNSKIKKQTLVTVCEGVSQSKNIYQNLISOFL 180

Db 200 LHYLQVNSTISVRDVFQYVDTNFTPLDNVLSVFLYSSSD 239
QY 181 LHYLQVNSTISVRDVFQYVDTNFTPLDNVLSVFLYSSSD 220

RESULT 7
ID US-08-570-923-23 STANDARD; PRT; 215 AA.
XX
AC xxxxxx
XX
XX
DT
DE
DE Sequence 23, Application US/08570923
XX
XX Sequence 23, Application US/08570923
XX Patent No. 5677430
CC
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jergen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
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CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 215 AA; 24151 MW; 261175 CN;

Query Match 74.9%; Score 1189; DB 1; Length 215;
Best Local Similarity 73.8%; Pred. No. 4.85e-94;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;

Db 14 TTSRSFYLTATLALCLVFTVATIMVLVQRTDSINSPDNVPLKGGNCSEDLCLIKR 73
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Db 74 APEKSWAYLQVAKHLNNTKLSWNKDGILLHGVRYODGNLIVQFGLYFIICQLQFLVQCP 133
QY 79 TPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQFGLYFIICQLQFLVQCS 138

Db 134 NNSVDLKLLELLINKHKQALVTVCESGMOTKHVYQNLQSFLLDYLVQVNTTISVNDTFQ 193
QY 139 NHSVDTLQLLINSKIKKQTLVTVCEGVSQSKNIYQNLQFLHLYLVQVNSTISVRDVFQ 198

Db 194 YDTSTFPLENVLSIFLYSNSD 215
QY 199 YVDTNFTPLDNVLSVFLYSSSD 220

RESULT 8
ID US-08-225-989-23 STANDARD; PRT; 215 AA.
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AC xxxxxx
XX
XX
DT
DE
DE Sequence 23, Application US/08225989
XX
XX Sequence 23, Application US/08225989
XX Patent No. 5480981
CC
CC GENERAL INFORMATION:
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Query Match 74.9%; Score 1189; DB 2; Length 215;
Best Local Similarity 73.8%; Pred. No. 4.85e-94;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;

CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 234 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 234 AA; 26017 MW; 308679 CN;

Query Match 74.9%; Score 1189; DB 1; Length 234;
Best Local Similarity 73.8%; Pred. No. 4.85e-94;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;
Db 33 TTSRSYFYLTTALCLVFTVATIMLVVQRTDSIPNSPDNVLKGGNCSEDLCLILKR 92
QY 20 STSRSYFLSTTAL-VCLVVAIVAILVLVQKDDSTPNTTEKAPLKGNCSEDLFCTLKS 78
Db 93 APFKSWAYLQVAKHLNKTLSWKNKGILHGVRVYQDGNLVIOFPGLYFICQLQFLVQCP 152
QY 79 TPKSKSWAYLQVSKHLNKTLSWNEGTIHLIYQDGNLVIOFPGLYFIVCQLQFLVQCS 138
Db 153 NNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLQSOFLLDYLOVNTTISVNVDTFQ 212
QY 139 NNSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNLQSOFLLHYLQVNSTISVRVDNFQ 198
Db 213 YDSTTFPLENVLISFLYSNSD 234
QY 199 YVDNTTFPLDNVLSVFLYSNSD 220

RESULT 12
ID US-08-580-014-8 STANDARD; PRT; 234 AA.

XX xxxxxx

Sequence 8, Application US/08580014

Sequence 8, Application US/08580014
Patent No. 5753203

GENERAL INFORMATION:

APPLICANT: Goodwin, Raymond G.

APPLICANT: Smith, Craig A.

APPLICANT: Armistage, Richard J.

APPLICANT: Gruss, Hans-Jurgen

TITLE OF INVENTION: NO. 5753203el Cytokine That Binds CD30

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Seese, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580,014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 234 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 234 AA; 26017 MW; 308679 CN;

Query Match 74.9%; Score 1189; DB 2; Length 234;
Best Local Similarity 73.8%; Pred. No. 4.85e-94;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;

Db 33 TTSRSYFYLTTALCLVFTVATIMLVVQRTDSIPNSPDNVLKGGNCSEDLCLILKR 92
QY 20 STSRSYFLSTTAL-VCLVVAIVAILVLVQKDDSTPNTTEKAPLKGNCSEDLFCTLKS 78

Db 93 APFKSWAYLQVAKHLNKTLSWKNKGILHGVRVYQDGNLVIOFPGLYFICQLQFLVQCP 152
QY 79 TPKSKSWAYLQVSKHLNKTLSWNEGTIHLIYQDGNLVIOFPGLYFIVCQLQFLVQCS 138

Db 153 NNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLQSOFLLDYLOVNTTISVNVDTFQ 212
QY 139 NNSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNLQSOFLLHYLQVNSTISVRVDNFQ 198

Db 213 YDSTTFPLENVLISFLYSNSD 234

QY 199 YVDNTTFPLDNVLSVFLYSNSD 220

RESULT 13

ID US-08-580-014-21 STANDARD; PRT; 130 AA.

XX xxxxxx

Sequence 21, Application US/08580014

CC Sequence 21, Application US/08580014
CC Patent No. 5753203
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580,014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 130 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein fragment
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC IMMEDIATE SOURCE:
CC CLONE: mUCD30 fragment (PRELIM)
CC SEQUENCE 130 AA: 14522 MW; 97051 CN;

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Best Local Similarity 99.2%; Pred. No. 9.09e-73;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MQVQPGSVASPRWRSTPRWSTRSYFLSTALVCLVAVAILLVVQKDSPTNTEK 60

Qy 1 MQVQPGSVASPRWRSTPRWSTRSYFLSTALVCLVAVAILLVVQKDSPTNTEK 60

Db 61 APLKGNCSDELFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIQV 120

Qy 61 APLKGNCSDELFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIQV 120
Db 121 FPGLYFIVCQ 130
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RESULT 14
ID US-08-225-989-21 STANDARD; PRT; 130 AA.
XX
AC xxxxxx
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DE Sequence 21, Application US/08225989
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CC Sequence 21, Application US/08225989
CC Patent No. 5480981
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
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CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 130 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein fragment

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CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 130 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein fragment
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC IMMEDIATE SOURCE:
CC CLONE: mucD30 fragment (PRELIM)
CC SQ SEQUENCE 130 AA; 14522 MW; 97051 CN;

Query Match          59.9%; Score 951; DB 1; Length 130;
Best Local Similarity 99.2%; Pred. No. 9,09e-73;
Matches 129; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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WIRE (TM)

Release 3.1A John F. Collins, Blocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:47:00 1999; MasPar time 11.13 Seconds
Tabular output not generated.
792.255 Million cell updates/sec

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Scoring table: PAM 150
Gap 11
Searched: 122810 seqs, 40068593 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
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1:pir1 2:pir2 3:pir3 4:pir4
Statistics: Mean 44.623; Variance 89.098; scale 0.501

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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4	115	7.2 560 2 D69649 probable long-chain-f	4.77e-03
5	113	7.1 279 2 A53062 Fas ligand - mouse	9.01e-03
6	111	7.0 499 2 A55346 phosphoprotein phosph	1.69e-02
7	109	6.9 397 2 B27496 proteinase inhibitor	3.16e-02
8	104	6.5 619 2 S54636 probable membrane pro	1.46e-01
9	103	6.5 693 2 A49228 sodium-dependent phos	1.97e-01
10	101	6.4 278 2 A49266 fas ligand - rat	3.58e-01
11	100	6.3 598 2 S51456 probable membrane pro	4.80e-01
12	99	6.2 249 2 G64081 luc operon regulatory	6.44e-01
13	99	6.2 259 2 C36819 C11 protein - rabbit	6.44e-01
14	98	6.2 397 2 I48717 proteinase inhibitor	8.62e-01
15	97	6.1 560 2 S27874 steroid hormone recep	1.15e+00
16	95	6.0 445 2 S58282 dTDP-glucose 4-6-dehy	2.04e+00
17	96	6.0 4910 2 S64942 probable membrane pro	1.53e+00
18	94	5.9 281 2 I38707 Fas ligand - human	2.70e+00
19	93	5.9 418 2 S11678 cyclin A - African cl	3.58e+00
20	94	5.9 434 2 T02407 heme A farnesyltransf	2.70e+00
21	94	5.9 469 2 T01579 heme A:farnesyltransf	2.70e+00
22	94	5.9 476 2 A48664 toxin synthesis trans	2.70e+00
23	93	5.9 575 2 G69834 transporter binding p	3.58e+00

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25	92	5.8	197	2	JH0309	tumor necrosis factor	4.73e+00
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27	92	5.8	407	2	J01654	SFRI protein - human	4.73e+00
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41	89	5.6	428	1	S32804	GTP-binding protein o	1.07e+01
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ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-1999
ACCESSIONS B40710
REFERENCE A40710
#authors Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, G.R.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Grabstein, K.H.; Gliniak, B.; McAllister, I.B.; Fanslow, W.; Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Arnitage, R.J.
#journal Cell (1993) 73:1349-1360
#title CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand defines an emerging family of cytokines with homology to TNF.
#cross-references MUID:93313964
#accession B40710
#status preliminary
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#cross-references GB:L09754; NID:G349288; PID:G349289
KEYWORDS cytokine receptor; membrane protein; surface antigen
SUMMARY #length 239 #molecular-weight 26519 #checksum 3403
Query Match 100.0%; Score 1588; DB 2: Length 239;
Best Local Similarity 100.0%; Pred. No. 2.80e-299;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

#molecule_type mRNA									
#residues 1-239 ##label SMI									
#cross-references GB:I09754; NID:G349288; PID:G349289									
KEYWORDS cytokine receptor; membrane protein; surface antigen									
#length 239 #molecular-weight 26519 #checksum 3403									
SUMMARY									
Query Match 100.0%; Score 1588; DB 2: Length 239;									
Best Local Similarity 100.0%; Pred. No. 2,80e-299;									
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Db	20	MQVPGSVASPRWRTPWRS	SRSYFLSTTALVCLVAVAILLVVQKDKSTPTTTEK	79					
QY	1	MQVPGSVASPRWRTPWRS	SRSYFLSTTALVCLVAVAILLVVQKDKSTPTTTEK	60					
Db	80	APLKGNCSEDLFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIYQ	139						
QY	61	APLKGNCSEDLFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIYQ	120						
Db	140	FPGLYFIVCQLQFLVQCNSHSDLTLLQLINSKIKQILVIVCESGVQSKNIYQNSQL	199						
QY	121	FPGLYFIVCQLQFLVQCNSHSDLTLLQLINSKIKQILVIVCESGVQSKNIYQNSQL	180						
Db	200	LHYLQVNSTISVRVDFVNTFFPLDNVLSVFLYSSSD	239						
QY	181	LHYLQVNSTISVRVDFVNTFFPLDNVLSVFLYSSSD	220						


```
RESULT 2
ENTRY A40710 #type complete
TITLE CD30 ligand -human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change
17-Mar-1999
ACCESSIONS A40710
REFERENCE Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah,
#authors T.; Baker, E.; Sutherland, G.R.; Brannan, C.I.; Copeland,
N.G.; Jenkins, N.A.; Grabstein, K.H.; Gliniak, B.;
McAlister, I.B.; Fanslow, W.; Alderson, M.; Falk, B.;
Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage,
R.J.
#journal Cell (1993) 73:1349-1360
#title CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor
whose ligand defines an emerging family of cytokines with
homology to TNF.
#cross-references MUID:93313964
#accession A40710
#status Preliminary
#molecule_type mRNA
#residues 1-234 #label SMI
#cross-references GB:L09753; NID:g349277; PID:g349278
KEYWORDS cytokine receptor; membrane protein; surface antigen
SUMMARY #length 234 #molecular-weight 26017 #checksum 1088
Query Match 74.9%; Score 1189; DB 2; Length 234;
Best Local Similarity 73.8%; Pred. No. 3.58e-215;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;
Db 33 TTSRSYFLTTALCLVETVATIMVLYVQRTDSIPNSPDNVPLKGGNCSEDLICILKR 92
QY 20 STSRSYFLSTAL-VCLVVAIIIVLVQKDSIPNTERAPLKGKNCSEDLFCILKS 78
Db 93 APFKSWAYLQVAKHLNKLKSNKDGILHGVRYQDGNLVIQPPGLYFIICQLQFLVQCP 152
QY 79 TPKSKSWAYLQVSKHLNKLKSNWEDGTIHLIYQDGNLVIQPPGLYFIICQLQFLVQCS 138
Db 153 NNSVDLKLLELHINKHKKALVTVCSGQKTHVYQNLQFLDYLVQNTTISVNVDTFO 212
QY 139 NHSVDTLLOLLINSKIKKQTLVTVCSGQSKNIYQNLQFLHYLVQNVSTISVRVDNEQ 198
Db 213 YDTSFTFPLENVLSIFLYNSD 234
QY 199 YVDNTFTPLDNVLSVFLSSD 220

RESULT 3
ENTRY S52570 #type complete
TITLE phosphoprotein phosphatase (EC 3.1.3.16) 5, catalytic subunit
- human
ALTERNATE_NAMES serine/threonine phosphatase PP5
ORGANISM #formal_name Homo sapiens #common_name man
DATE 01-Aug-1995 #sequence_revision 02-Jul-1996 #text_change
17-Mar-1999
ACCESSIONS S52570; PC4136
REFERENCE Chen, M.X.; McPartlin, A.E.; Brown, L.; Chen, Y.H.; Barker,
#authors H.M.; Cohen, P.T.W.
#journal EMBO J. (1994) 13:4278-4290
#title A novel human protein serine/threonine phosphatase, which
possesses four tetratricopeptide repeat motifs and
localizes to the nucleus.
#cross-references MUID:95009929
#accession S52570
#molecule_type mRNA
#residues 7-498 #label CH2
#cross-references EMBL:S73586; EMBL:X89416
#experimental_source teratocarcinoma cell line NTERA-2
REFERENCE PC4136
#authors Xu, X.L.; Lagercrantz, J.; Zickert, P.; Bajjalica-Lagercrantz,
```

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S.; Zetterberg, A.
Biochem. Biophys. Res. Commun. (1996) 218:514-517
Chromosomal localization and 5' sequence of the human protein
serine/threonine phosphatase 5' gene.
#journal PC4136
#title
#accession
#molecule_type mRNA
#residues 1-37 #label XUX
#cross-references EMBL:X92121; NID:gl177477; PID:e205526; PID:gl177478
#experimental_source fetal brain
GENETICS
#gene GDB:PPP5C; PPP5; PP5
#cross-references GDB:I36857
#map_position 19q13.3-19q13.3
FUNCTION
#description catalyzes the hydrolytic dephosphorylation of
protein-phosphoserine and protein-phosphothreonine
plays a role in the regulation of RNA synthesis and mitosis
#superfamily phosphoprotein phosphatase homology;
phosphoesterase core homology; tetratricopeptide repeat
homology
KEYWORDS iron; nucleus; phosphoric monoester hydrolase; zinc
FEATURE
28-61
62-95
62-95
96-129
204-467
236-305
242,244,271
271,303,332,426
274,304,450
275,399
SUMMARY #length 498 #molecular-weight 56820 #checksum 5353
Query Match 7.4%; Score 117; DB 2; Length 498;
Best Local Similarity 23.9%; Pred. No. 2.51e-03;
Matches 21; Conservative 29; Mismatches 32; Indels 6; Gaps 6;
Db 208 CAYQILVQ-VKEVLS-KLSTLVETTLKETIKIVC-GDTGQ-FYDLLNIFELNGLPSET 263
QY 129 CQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLQFLHYLVQNS 188
Db 264 NPVI-ENG-DEVDRGSGFSEVILTLFGF 289
QY 189 TISVRVDNFQIVDTNFTPLDNVLSVFLY 216

RESULT 4
ENTRY D69649 #type complete
TITLE Probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) lcfa
- Bacillus subtilis
ORGANISM #formal_name Bacillus subtilis
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
05-Feb-1999
ACCESSIONS D69649
REFERENCE A69580
#authors Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Chim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandl, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.;
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Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Mostl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetellev, D.; Porwollik, S.; Prescott, A.M.; Prescecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Wambutt, R.; Wedler, E.; Wedler, H.; Weitzneggert, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zmistein, E.; Yoshikawa, H.; Danchin, A.

Nature (1997) 390:249-256

The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

#journal
#title

#cross-references MUID:98044033
 #accession D69649
 ##status preliminary; nucleic acid sequence not shown;
 translation not shown

[illegible]

#gene
 #superfamily acetate--CoA ligase homology
 #acid-thiol ligase
 #KEYWORDS
 #lcfA
 #ACASSIFICATION
 #NETICS

70-549
#domain acetate--CoA ligase homology #label ACL
#length 560 #molecular-weight 62691 #checksum 4760

Query Match	7.28;	Score 115;	DB 2;	Length 560;
Best Local Similarity	27.38;	Pred. No. 4.77e-03;		
Matches	27;	Conservative	28;	Mismatches 38;
			Indels	6;
			Gaps	6;

93 GVLF-AGGIVVQTNPLY-TEHELEYQLRDAQSVIITIDLLFPKAKMKTLSIVDQILIT 150
|::: |::: || |::: :: |:: |::|::|:: |:: |:: |:: |:: |:: |:: |:: |::
109 GLIIQDGNLIVFPPGLYFIVCQLFLVQCNSHSDLTQLQLINSIKKQTLYTVCESGVQ 168

[illegible]

0123456789ABCDEFGHIJKLMNOPQRSTUVWXYZ

5	RESULT	
	TITLE	A53062 #type complete
	TITLE	Fas ligand - mouse
	TITLE	#formal_name Mus musculus #common_name house mouse
	ORGANISM	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
	DATE	10-Sep-1997

10-Sep-1997
A53062
A53062
Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.;
#authors Copeland, N.G.; Suda, T.; Nagata, S.
#journal Cell (1994) 76:969-976
#title Generalized lymphoproliferative disease in mice, caused by a
point mutation in the Fas ligand.
#cross-references MUID:94185175

```

#accession A53062
#status preliminary
#molecule_type mRNA
#residues 1-279 ##label TAK
#cross-references GB:006948; NID:g473564; PID:g473565
#length 279 ##molecular-weight 31442 #checked
#MNAME

```

```
MMARY
#length 279 #molecular-weight 31442 #checksum 3291
```

Query Match	7.1%	Score 113;	DB 2;	Length 279;
Best Local Similarity	32.3%;	Pred. 9.01e-03;		
Matches	20;	Conservative 14;	Mismatches 24;	Indels 4; Gaps
Db	145	AHUTGPHRSRISPLEWEDTYGTALISGVYKKGGLVINETGLYFYVSKYVFRGQSCNNOP	204	
Qy	86	AYLQVSKHLNNTKLSWNE-DT--IHGLIYQGNLIYQFPGLYFYVCVQLQFLVQ-CSNHS	141	
Db	205	LN	206	
Qy	142	VD	143	

RESULTS

6	RESULTS
ENTRY	A5346 #type complete
TITLE	phosphoprotein phosphatase (EC 3.1.3.16) ppt - rat
ORGANISM	#formal_name Rattus norvegicus #common_name Norway rat
DATE	10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-1999

ACCESSIONS
REFERENCE

#authors
Becker, W.; Kentrup, H.; Klumpp, S.; Schultz, J.E.; Joost,
H.G.

#journal J. Biol. Chem. (1994) 269:22586-22592
#title Molecular cloning of a protein serine/threonine phosphatase containing a putative regulatory tetratricopeptide repeat domain.
#author Hsu C., Chen Y.-N. S.

#cross-references MUID:94357899
#accession A55346

```

##status      preliminary
##molecule_type  mRNA
##residues    1-499 ##label BEC

```

```

##residues      1-499  ##label  SEC
##cross-references  GB:X77237
##note
      authors translated the codon AAG for residue 53 as Gln,
      and GTA for residue 496 as Leu

```

CLASSIFICATION
#superfamily phosphoprotein phosphatase homology;
phosphoesterase core homology; tetratricopeptide repeat
homology

KEYWORDS
phosphoric monoester hydrolase

KEYWORDS	
FEATURE	
28-61	
62-95	
96-129	
204-460	
236-300	
SUMMARY	

Query Match	7.08	Score 111	DB 2	Length 499
Best Local Similarity	25.88	Pred. No. 1.69e-02		
Matches	23	Conservative	28	Mismatches 30
			Indels	8
			Gaps	8

Db 208 CAYQILVQ-VKE-V-LCKLSTLVETTLKETEKITVC-GDTHCQ-FYDLLNIFEINGLPSE 262
| : ||| : | | : :: : ||| : :: : | : | : | :
Ov 129 COLOFLVCSNHSDLL-TIOLLINSKIKKOTLVTVCEGVSOKNIYONI-SOFILHYILOVN 187

QY	129	CQLQFLVQCNSHSDVL-ILQELLINSKIRKQTL
Db	263	TNPYI-FNG-DFVDRGFSFSEVILTLFGF 289
QY	188	STISVRVDNFOYVDNTEPLDNVLSVEYL 216

1885

```

7
RESULT      B27496      #type fragment
ENTRY       protease_inhibitor nexin 1 precursor - rat (fragment)
TITLE       gila-derived nexin (GDN)
ALTERNATE_NAMES #formal_name Rattus norvegicus #common_name Norway rat
ORGANISM    30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
DATE        05-Dec-1998

```

ACCESSIONS	03-DEC-1998	
REFERENCE		
	B27496; A34538; A42351; B42351; C42351	
	A90519	

350013	Sommer, J.; Gloor, S.M.; Rovelli, G.F.; Hofsteenge, J.; Nick, H.; Meier, R.; Monard, D.
#authors	Biochemistry (1987) 26:6407-6410
#journal	CDNA sequence coding for a rat cilia-derived nexin and its
#title	

3

```

ACCESSIONS      A49266
REFERENCE        A49266
#authors        Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
#journal        Cell (1993) 75:1169-1178
#title          Molecular cloning and expression of the Fas ligand, a novel
                member of the tumor necrosis factor family.
#cross-references MIMD:94084792
#accession      A49266
#status         preliminary
#molecule_type mRNA
#residues       1-278 #label SUD
#cross-references GB:U03470; NID:G440178; PID:G440179
KEYWORDS         glycoprotein; transmembrane protein
SUMMARY          #length 278 #molecular-weight 31140 #checksum 9586

Query Match      6.4%; Score 101; DB 2; Length 278;
Best Local Similarity 33.3%; Pred. No. 3.58e-01;
Matches 16; Conservative 13; Mismatches 15; Indels 4; Gaps 3;

Db 157 LEWEDYGTALISGVKKGLVINEAGLYFVYKVFYRGSCNSQPL 204
QY 99 LSWNE-DGI--IHGLYQDGNLIVQPFGLYFIVCQLQFLVQ-CNSHSV 142

RESULT 11
ENTRY      S51456 #type complete
TITLE      Probable membrane protein YLR237w - yeast (Saccharomyces
            cerevisiae)
ALTERNATE_NAMES hypothetical protein I8083.2
ORGANISM      #formal_name Saccharomyces cerevisiae
DATE          23-Feb-1995 #sequence_revision 12-May-1995 #text_change
            06-Feb-1998
ACCESSIONS      S51456
REFERENCE        S51443
#authors        Hallsworth, K.
#submission     submitted to the EMBL Data Library, December 1994
#description    The sequence of S. cerevisiae cosmid 8083.
#accession      S51456
#molecule_type DNA
#residues       1-598 #label HAL
#cross-references EMBL:U19027; NID:G609363; PID:G609365; MIPS:YLR237w
GENETICS        SGD:TH17
#gene           SGD:TH17
#cross-references SGD:S0004227; MIPS:YLR237w
#map_position 12R
KEYWORDS         transmembrane protein
FEATURE
78-94          #domain transmembrane #status predicted #label TM1\
116-132        #domain transmembrane #status predicted #label TM2\
174-190        #domain transmembrane #status predicted #label TM3\
199-215        #domain transmembrane #status predicted #label TM4\
280-296        #domain transmembrane #status predicted #label TM5\
398-414        #domain transmembrane #status predicted #label TM6\
485-501        #domain transmembrane #status predicted #label TM7\
SUMMARY          #length 598 #molecular-weight 66903 #checksum 8385

Query Match      6.3%; Score 100; DB 2; Length 598;
Best Local Similarity 30.2%; Pred. No. 4.80e-01;
Matches 19; Conservative 16; Mismatches 25; Indels 3; Gaps 3;

Db 334 FGLSLVLSQMSYTSINCFASGMDIAGLLPKYVDIKRGALFAACVSWACLPWNFNSSS 393
QY 121 FFLGLYFIVCQLQFLV-QCS-NHSVDLTQLLINSKIKKQTLTVTCES-GVQSKNIYQNL 177

Db 394 TFL 396
QY 178 QFL 180

RESULT 12
ENTRY      G64081 #type complete
TITLE      fuc operon regulatory protein homolog - Haemophilus
            influenzae (strain Rd RW20)

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```

ORGANISM        #formal_name Haemophilus influenzae
DATE            18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
                24-Oct-1997
ACCESSIONS      G64081
REFERENCE        A64000
#authors        Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
                Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
                Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
                Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
                Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
                J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
                M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
                D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
                J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
                Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal        Science (1995) 269:496-512
#title          Whole-genome random sequencing and assembly of Haemophilus
                influenzae Rd.
#cross-references MIMD:95350630
#accession      G64081
#status         nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues       1-249 #label TIGR
#cross-references GB:U32744; GB:L42023; NID:G1573608; PID:G1573609;
                TIGR:HI0615
SUMMARY          #length 249 #molecular-weight 28163 #checksum 2069

Query Match      6.2%; Score 99; DB 2; Length 249;
Best Local Similarity 19.6%; Pred. No. 6.44e-01;
Matches 21; Conservative 35; Mismatches 46; Indels 5; Gaps 5;

Db 64 SFFQTRKHINATA-KRHIAQKALDLYENAVIGLDASTSYFYALMP-DIPCTVVTNSM 121
QY 86 AYLOVSKHLANTKLSWEDGTIHLIYQDGNLIVQFGL-YFIVCQLQFLVQCSNHSVDL 144

Db 122 FNINALVN-KSNVKTIVTGGVYSKAYEAFYGLPELLEQLRLHINFSV 167
QY 145 -TIQLLINSKIKKQTLTVTCESGVQSKNIYQNLQFLHLHYLQVNSTI 190

RESULT 13
ENTRY      C36819 #type complete
TITLE      C11 protein - rabbit fibroma virus
ORGANISM      #formal_name rabbit fibroma virus, Shope fibroma virus
DATE          23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change
                21-Aug-1998
ACCESSIONS      C36819
REFERENCE        A41700
#authors        Strayer, D.S.; Jerng, H.H.; O'Connor, K.
#journal        Virology (1991) 185:585-595
#title          Sequence and analysis of a portion of the genomes of Shope
                fibroma virus and malignant rabbit fibroma virus that is
                important for viral replication in lymphocytes.
#accession      C36819
#status         translation not shown
#molecule_type DNA
#residues       1-259 #label STR
#cross-references GB:M32743
CLASSIFICATION  #superfamily vaccinia virus D1OR protein; mutt domain
                homology
FEATURE
123-157        #domain mutt domain homology #label MUTT
SUMMARY          #length 259 #molecular-weight 30411 #checksum 5504

Query Match      6.2%; Score 99; DB 2; Length 259;
Best Local Similarity 28.3%; Pred. No. 6.44e-01;
Matches 15; Conservative 19; Mismatches 16; Indels 3; Gaps 3;

Db 147 EINIDSKDIYD-SRFFVH-LFIEDLLSNRIYETILFLGKTLTSLHNNFL 197
QY 164 ESGVQSKNIYQNLQFLHLHYLQVNSTISVRV-DNFQYVDYTNFPLDNLVSLVFL 215

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RESULT 14
ENTRY
TITLE      #type complete
ORGANISM   proteinase inhibitor nexin I precursor - mouse
DATE       #formal_name Mus musculus #common_name house mouse
           02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I48717; S70772; S35731
REFERENCE   I48717; S70772
#authors   Vassalli, J.D.; Huarte, J.; Bosco, D.; Sappino, A.P.;
           Sappino, N.; Velard, A.; Wohliwend, A.; Erno, H.; Monard,
           D.; Belin, D.
#journal   EMBO J. (1993) 12:1871-1878
#title     Protease-nexin I as an androgen-dependent secretory product
           of the murine seminal vesicle.
#cross-references MUID:93259128
#accession I48717
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-397 #label RES
#cross-references EMBL:X70296; NID:g551064; PID:g551065
#accession S70772
#status    nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues  1-86 #label VAS
#cross-references EMBL:X70946; NID:g57930; PID:g57931
#note      the nucleotide sequence was submitted to the EMBL Data
           Library, February 1993
GENETICS
#gene      PN-1
CLASSIFICATION #superfamily antithrombin III
KEYWORDS     serine proteinase inhibitor
FEATURE
1-19         #domain signal sequence #status predicted #label SIG\
20-397       #product proteinase inhibitor nexin I #status predicted
           #label MAT
SUMMARY      #length 397 #molecular-weight 44207 #checksum 3957
Query Match 6.2%; Score 98; DB 2; Length 397;
Best Local Similarity 28.2%; Pred.No. 8,62e-01;
Matches 31; Conservative 26; Mismatches 49; Indels 4; Gaps 4;
Db 285 VPKRMQLVPKFTAVAQTDLKEPLKALGITE-MFEPSKANFTKTRSESLHYSHILQKAK 343
: : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Qy 40 VAILLVVQKKDTPNTEKAPKGGNCSEDLCTLKSTPSKKSWA-YLQVSKHLNNTK 98
: : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Db 344 IEVSEDTGKASAA-TTALIAKSPFPFIV-DRPFLFSIRHNPTGAILFL 391
: : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Qy 99 LSWNEDGTHGLIYQDGNLIVQPGLYFIVCQLFLVQCSNHSVDLTQL 148
: : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||

RESULT 15
ENTRY
TITLE      #type complete
ORGANISM   steroid hormone receptor homolog LRH-1 - mouse
DATE       #formal_name Mus musculus #common_name house mouse
           17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
ACCESSIONS S27874
REFERENCE   S27874
#authors   Tugwood, J.D.; Issemann, I.; Green, S.
#submission submitted to the EMBL Data Library, February 1992
#description LRH-1: A nuclear hormone receptor active in the absence of
           exogenous ligands.
#accession S27874
#molecule_type mRNA
#residues  1-560 #label TUG
#cross-references EMBL:M81385; NID:g198872; PID:g198875
FUNCTION
#description transcription regulation; probably a steroid hormone receptor
CLASSIFICATION #superfamily steroid hormone receptor Ad4BP; erba
KEYWORDS       transforming protein homology
           DNA binding; nucleus; steroid hormone receptor; transcription
           factor; zinc finger
FEATURE
```

```
105-478      #domain erBA transforming protein homology #label ERBA\
107-127      #region zinc finger CCCC motif\
143-167      #region zinc finger CCCC motif\
SUMMARY      #length 560 #molecular-weight 64020 #checksum 4722
Query Match 6.1%; Score 97; DB 2; Length 560;
Best Local Similarity 22.7%; Pred.No. 1.15e+00;
Matches 27; Conservative 38; Mismatches 44; Indels 10; Gaps 7;
Db 423 FLVTGEHVDYTIISHTSEVAFNLLSLAQELVLRSLQDQREFVC-LKFLVLFSSDYK 481
: : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Qy 87 YLQVSKHLNNTKLSWNEDGTHGLIYQDGNLIVQPGLYF----IVCQLFLVQCSNHSV 142
: : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Db 482 NLENLQL-VEG-VQEOVNAALDYTCNYPQQTQKFGQLLR-LPEIRAIKQAEEDYLY 537
: : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Qy 143 DL-TLQLLINSKIKKQLTVTCESGV-QSKNIYQNLISQFLHYLVQVNSTISVRVDNFQY 199
: : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Search completed: Fri Aug 13 16:47:21 1999
Job time : 21 secs.
```

W P S R E L

(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:48:53 1999; MasPar time 7.81 Seconds
Tabular output not generated.

Title: >US-09-079-785-19
Description: (1-220) from US09079785.pep
Perfect Score: 1588
Sequence: 1 MQVQGSVASPWRSPRPS.....DNTFFLDNVLVSFLYSSD 220
Scoring table: PAM 150
Gap 11
Searched: 77977 seqs, 28268293 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot37
1:swissprot
Statistics: Mean 45.658; Variance 78.252; scale 0.583

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1588	100.0	239	1 CD3L_MOUSE	CD30 LIGAND (CD30-L).	0.00e+00
2	1189	74.9	234	1 CD3L_HUMAN	CD30 LIGAND (CD30-L) (2.34e-250
3	117	7.4	499	1 PP5_HUMAN	SERINE/THREONINE PROTE	2.39e-04
4	115	7.2	560	1 LCFA_BACSU	LONG-CHAIN-FATTY-ACID-	4.98e-04
5	113	7.1	279	1 FASL_MOUSE	FAS ANTIGEN LIGAND.	1.03e-03
6	111	7.0	499	1 PP5_RAT	SERINE/THREONINE PROTE	2.12e-03
7	109	6.9	397	1 GDN_RAT	GLIA DERIVED NEXIN PRE	4.31e-03
8	104	6.5	260	1 VD10_SFVKA	PROTEIN D10.	2.47e-02
9	101	6.4	278	1 FASL_RAT	FAS ANTIGEN LIGAND.	6.84e-02
10	100	6.3	598	1 TH17_YEAST	THIAMINE TRANSPORTER.	9.56e-02
11	99	6.2	249	1 FCUR_HAEIN	L-FUCOSE OPERON ACTIVA	1.33e-01
12	98	6.2	397	1 GDN_MOUSE	GLIA DERIVED NEXIN PRE	1.86e-01
13	97	6.1	499	1 FTF_MOUSE	ALPHA-1-FETOPROTEIN TR	2.58e-01
14	95	6.0	233	1 TNFA_TRIVU	TUMOR NECROSIS FACTOR	4.93e-01
15	95	6.0	773	1 L119_DROME	LIN-19 HOMOLOG PROTEIN	4.93e-01
16	94	5.9	281	1 FASL_HUMAN	FAS ANTIGEN LIGAND (AP	6.79e-01
17	93	5.9	418	1 CGAL_XENLA	G2/MITOTIC-SPECIFIC CY	9.34e-01
18	93	5.9	1202	1 YE01_SCHPO	HYPOTHETICAL 138.5 KD	9.34e-01
19	92	5.8	197	1 TNFB_RABIT	LYMPHOTOXIN-ALPHA PREC	1.28e+00
20	92	5.8	436	1 VU10_HSV6U	U10 PROTEIN.	1.28e+00
21	91	5.7	427	1 KTA_HAEIN	3-DEOXY-D-MANNO-OCTULO	1.75e+00
22	90	5.7	746	1 YUS8_CAEEL	HYPOTHETICAL 83.6 KD P	2.38e+00
23	91	5.7	2787	1 TELL_YEAST	TELOMER LENGTH REGULAT	1.75e+00

24	89	5.6	233	1	TNFA_MACFA	TUMOR NECROSIS FACTOR	3.24e+00
25	89	5.6	375	1	GM12_SCHPO	ALPHA-1,2-GALACTOSYLTR	3.24e+00
26	89	5.6	427	1	7SBG_SOYBN	BASIC 7S GLOBULIN PREC	3.24e+00
27	89	5.6	428	1	OBG_BACSU	SPOB8 ASSOCIATED GTP-B	3.24e+00
28	89	5.6	599	1	TH17_YEAST	PUTATIVE THIAMINE TRAN	3.24e+00
29	89	5.6	1156	1	JAK1_CYPCA	TYROSINE-PROTEIN KINAS	3.24e+00
30	89	5.6	1191	1	TOP2_ASFM2	DNA TOPOISOMERASE II (3.24e+00
31	89	5.6	1636	1	YN37_YEAST	HYPOTHETICAL 186.8 KD	3.24e+00
32	87	5.5	202	1	TNFB_RAT	LYMPHOTOXIN-ALPHA PREC	5.92e+00
33	88	5.5	349	1	GBT1_CANFA	GUANINE NUCLEOTIDE-BIN	4.38e+00
34	88	5.5	349	1	GBT1_MOUSE	GUANINE NUCLEOTIDE-BIN	4.38e+00
35	87	5.5	349	1	GBT_XENLA	GUANINE NUCLEOTIDE-BIN	5.92e+00
36	87	5.5	349	1	GBT1_BOVIN	GUANINE NUCLEOTIDE-BIN	5.92e+00
37	88	5.5	351	1	YZ39_METJA	HYPOTHETICAL PROTEIN M	4.38e+00
38	88	5.5	353	1	GBT2_BOVIN	GUANINE NUCLEOTIDE-BIN	4.38e+00
39	88	5.5	353	1	GBT2_MOUSE	GUANINE NUCLEOTIDE-BIN	4.38e+00
40	88	5.5	527	1	NU2M_ACACA	NADH-UBIQUINONE OXIDOR	4.38e+00
41	88	5.5	585	1	DCE2_RAT	GLUTAMATE DECARBOXYLAS	4.38e+00
42	88	5.5	585	1	DCE2_PIG	GLUTAMATE DECARBOXYLAS	4.38e+00
43	87	5.5	585	1	DCE2_MOUSE	GLUTAMATE DECARBOXYLAS	5.92e+00
44	88	5.5	769	1	SW16_KLJLA	REGULATORY PROTEIN SWI	4.38e+00
45	87	5.5	1580	1	SUR_HUMAN	SULFONYLUREA RECEPTOR.	5.92e+00

ALIGNMENTS

RESULT 1
ID CD3L_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CD30 LIGAND (CD30-L).
GN CD30LG OR CD30L.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-T-CELL;
RX MEDLINE; 93313964.
RA SMITH C.A., GRUESER H.-J., DAVIS T., ANDERSON D., FARRAH T.,
BAKER E., SUTHERLAND G.R., BRANNAN C.I., COPELAND N.G., JENKINS N.A.,
GRABSTEIN K.H., GLINKAR B., MCALISTER I.B., FANSLAW W., ALDERSON M.,
FAUK B., GIMPEL S., GILLIS S., DIN W.S., GOODWIN R.G., ARMITAGE R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
TNF".
RL CELL 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
CC EMBL; L09754; G349289; -.
CC PIR; B40710; B40710.
CC MGI; 883328; CD30L.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS50049; TNF_2; 1.
CC PFAM; PF00229; TNF; 1.
CC KW CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
CC DOMAIN 1 43
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 44 67
CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CC DOMAIN 68 239
CC EXTRACELLULAR (POTENTIAL).
CC CARBOHYD 75 75

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FT CARBOHYD 86 86 POTENTIAL.
FT CARBOHYD 114 114 POTENTIAL.
FT CARBOHYD 158 158 POTENTIAL.
FT CARBOHYD 194 194 POTENTIAL.
FT CARBOHYD 206 206 POTENTIAL.
SQ SEQUENCE 239 AA; 26519 MW; 1EB8A1D CRC32;

Query Match 100.0%; Score 1588; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
Matches 220; Conservative 0; Mismatches 0;

Db 20 MOVQPGSVASPRWRSTRSYFYLSTALVCLVAVAILVWQKSDTPNTTEK 79
QY 1 MOVQPGSVASPRWRSTRSYFYLSTALVCLVAVAILVWQKSDTPNTTEK 60

Db 80 APLKGGNCSEDLFCILKSPKSKWAYLQVSKHLNKLKSWNEDGTIHLIYQDGNLIQV 139
QY 61 APLKGGNCSEDLFCILKSPKSKWAYLQVSKHLNKLKSWNEDGTIHLIYQDGNLIQV 120

Db 140 FGLYFIVCOLQFLVQCSNHSVDLTQLILNSKIKKQTLVTVCSGVQSKNIYQNLQFL 199
QY 121 FGLYFIVCOLQFLVQCSNHSVDLTQLILNSKIKKQTLVTVCSGVQSKNIYQNLQFL 180

Db 200 LHYLQVNSTISVRVDFQVYDNTFPLDNLVSVLYSSSD 239
QY 181 LHYLQVNSTISVRVDFQVYDNTFPLDNLVSVLYSSSD 220

RESULT 2
ID CD3L_HUMAN STANDARD; PRT; 234 AA.
AC P32971;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CD30 LIGAND (CD30-L) (CD153 ANTIGEN).
GN CD30LG OR CD30L.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93313964.
RA SMITH C.A., GRUERS H.-J., DAVIS T., ANDERSON D., FARRAH T.,
RA BAKER E., SUTHERLAND G.R., BRANNAN C.I., COPELAND N.G., JENKINS N.A.,
RA GRABSTEIN K.H., GLINIAK B., MCALISTER I.B., FANSLAW W., ALDERSON M.,
RA FALK B., GIMPEL S., GILLIS S., DIN W.S., GOODWIN R.G., ARMITAGE R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF."
RL CELL 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry.
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd153.htm".
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CC -----
DR EMBL; L09753; G349278;
DR PIR; A40710; A40710.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR PFAM; PF00229; TNF; 1.
KW CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
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FT DOMAIN 63 234 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 81 81 POTENTIAL.
FT CARBOHYD 109 109 POTENTIAL.
FT CARBOHYD 153 153 POTENTIAL.
FT CARBOHYD 189 189 POTENTIAL.
FT CARBOHYD 201 201 POTENTIAL.
SQ SEQUENCE 234 AA; 26017 MW; A77E97B1 CRC32;

Query Match 74.9%; Score 1189; DB 1; Length 234;
Best Local Similarity 73.8%; Pred. No. 2; Indels 1; Gaps 1;
Matches 149; Conservative 34; Mismatches 18;

Db 33 TTSRSYFYLSTALCLVETVATIMVLVQRTDSIPNSPDNPLKGGNCSEDLICILKR 92
QY 20 TTSRSYFYLSTAL-VCLVAVAILVWQKSDTPNTTEKAPLKGNCSEDLFCILKS 78

Db 93 APFKSKWAYLQVAKHLNKLKSNKDGILHGVRYQDGNLVQFGLYFIICOLQFLVQCP 152
QY 79 TPKSKWAYLQVSKHLNKLKSNWEDGTIHLIYQDGNLVQFGLYFIICOLQFLVQCS 138

Db 153 NNSVDLKLLELLINKHLKQALVTVCSGMOTKHVYQNLQFLDYLOVNTTISVNVDFQ 212
QY 139 NNSVDLTQLILNSKIKKQTLVTVCSGVQSKNIYQNLQFLDYLOVNTTISVNVDFQ 198

Db 213 YIDTSTFPLENLSIFLYSNSD 234
QY 199 YIDTSTFPLENLSIFLYSNSD 220

RESULT 3
ID PPP5_HUMAN STANDARD; PRT; 499 AA.
AC P53041; 016722;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN
DE PHOSPHATASE T) (PP-T) (PPT).
GN PPP5C OR PPP5.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE OF 7-499 FROM N.A.
RX MEDLINE; 95009929.
RA CHEN M.X., MCPARTLIN A.E., BROWN L., CHEN Y.H., BARKER H.M.,
RA COHEN P.T.W.;
RT "A novel human protein serine/threonine phosphatase, which possesses
RT four tetrapeptide repeat motifs and localizes to the nucleus."
RL EMBO J. 13:4278-4290(1994).
RN [2]
RP SEQUENCE OF 9-499 FROM N.A.
RC TISSUE-FETAL BRAIN;
RX MEDLINE; 96115607.
RA YONG W.H., UEKI K., CHOU D., REEVES S.A., VON DETMLING A.,
RA GUSSELL J.F., MOHREWEISER H.W., BUCKLER A.J., LOUIS D.N.;
RT "Cloning of a highly conserved human protein serine-threonine
RT phosphatase gene from the glioma candidate region on chromosome
RT 19q13.3."
RN [3]
RP SEQUENCE OF 1-37 FROM N.A.
RC TISSUE-FETAL BRAIN;
RX MEDLINE; 96144708.
RA XU X., LAGERCRANTZ J., ZICKERT P., BAJALICA-LAGERCRANTZ S.,
RA ZETTERBERG A.;
RT "Chromosomal localization and 5' sequence of the human protein
RT serine/threonine phosphatase 5' gene."
RL BIOCHEM. BIOPHYS. RES. COMMUN. 218:514-517(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS) OF 19-177.
RX MEDLINE; 98151343.
RA DAS A.K., COHEN P.W., BARFORD D.;
RT "The structure of the tetrapeptide repeats of protein
```

[illegible]

[illegible]

-!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-T SUBFAMILY.

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CC	-----	
DR	EMBL: X77337; G663080; --	
DR	PROSITE: PS00125; SER_THR_PHOSPHATASE; 1.	
DR	PFAM: PF00149; Sphosphatase; 1.	
DR	PFAM: PF00515; TPR; 2.	
DR	HSS: P53041; IAL1.	
DR	HYDROLASE; IRON; MANGANESE; NUCLEAR PROTEIN; REPEAT; TPR DOMAIN.	
KW	HYDROLASE; IRON; MANGANESE; NUCLEAR PROTEIN; REPEAT; TPR DOMAIN.	
FT	REPEAT 28 61	
FT	REPEAT 62 95	TPR 1.
FT	REPEAT 96 129	TPR 2.
FT	REPEAT 129 157	TPR 3.
FT	DOMAIN 200 499	CATALYTIC.
FT	METAL 242 242	IRON (BY SIMILARITY).
FT	METAL 244 244	IRON (BY SIMILARITY).
FT	METAL 271 271	IRON (BY SIMILARITY).
FT	METAL 303 303	IRON AND MANGANESE (BY SIMILARITY).
FT	ACT_SITE 304 304	MANGANESE (BY SIMILARITY).
FT	METAL 352 352	GENERAL ACID (BY SIMILARITY).
FT	METAL 427 427	MANGANESE (BY SIMILARITY).
SQ	SEQUENCE 499 AA; 56916 MW; 3BBA3664 CRC32;	

Query Match 7.0%; Score 111; DB 1; Length 499;
Best Local Similarity 25.8%; Pred. No. 2.12e-03;
Matches 23; Conservative 28; Mismatches 30; Indels 8; Gaps

129	CUQZF	EVQCSNHSVDL	-FLQLLINSLKRLVTV	CGSEGWQSRNIYQNDUSQF	LLHLYQVNI	18
Db	263	TNPYI	-FNG	-DFVDRGSEFSEV	ILTFGF	289
Ov	188	STISVYRDNFQYDVT	NTPLDNLSVELY	216		

QY 188 STSRVNDNFQVDFNTFFPLDNVLSVELY 216

RESULT 7
ID GDN RAT
STANDARD: DET: 107 AA

RESULT	7	
ID	GDN_RAT	
AC	P07092;	STANDARD;
		PRT; 397 AA.

```
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1).
GN P17 OR PNI.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88107544.
RA SOMMER J., GLOOR S.M., ROVELLI G.F., HOFSTEENGE J., NICK H.,
RA MEIER R., MONARD D.;
RT "GDN sequence coding for a rat glia-derived nexin and its homology
to members of the serpin superfamily.";
RL BIOCHEMISTRY 26:6407-6410(1987).
CC -1- FUNCTION: THIS GLYCOPROTEIN PROMOTES NEURITE EXTENSION AND IS A
CC SERINE PROTEASE INHIBITOR WITH ACTIVITY TOWARD THROMBIN, TRYPSIN,
CC AND UROKINASE. BINDS HEPARIN.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC -----
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CC -----
CC EMBL; M17784; G204284; -.
CC PIR; B27496; B27496.
CC PROSITE; PS00284; SERPIN; 1.
CC PRAM; PF00079; serpin; 1.
CC HSP; P05619; 1HLE.
KW SERINE PROTEASE INHIBITOR; SERPIN; HEPARIN-BINDING; NEURONE;
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 397 GLIA DERIVED NEXIN.
FT CARBOHYD 159 159 POTENTIAL.
FT ACT_SITE 364 365 REACTIVE BOND (POTENTIAL).
SQ SEQUENCE 397 AA; 44063 MW; D79E9B21 CRC32;

Query Match 6.9%; Score 109; DB 1; Length 397;
Best Local Similarity 30.1%; Pred. No. 4.31e-03;
Matches 31; Conservative 26; Mismatches 41; Indels 5; Gaps 5;

Db 285 VPKRMQLVLPKFTALQTDLKEPLKALGITE-MPEPSKANFAKITRSGESLHVSHLOKAK 343
QY 40 VAILLVVQKDKSTPTWTEKAPLKGNCSEDLCTLKSTPSKSWA-YLVQSKHLNNTK 98
Db 344 IYVEDGTKAADV-TTALIRSSPPWFIV-DRPFLP-CIRHN 383
QY 99 LSWNEDGTIEGLIVQDGNLIVQFPLGVFIVQLQFLVQCSNHS 141

RESULT 8
ID VD10_SFVKA STANDARD; PRT; 260 AA.
AC P32097;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DE 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE PROTEIN D10.
GN D10R.
OS SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).
OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; POXVIRIDAE; CHORDOPOXVIRINAE;
OC LEPORIPOXVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92074222.
RA STRAYER D.S., JERNIG H.H., O'CONNOR K.;
RT "Sequence and analysis of a portion of the genomes of Shope fibroma
RT virus and malignant rabbit fibroma virus that is important for viral
replication in lymphocytes.";
RL VIROLOGY 185:585-595(1991).
CC -1- SIMILARITY: TO PROTEINS WITH A CORE MUTT DOMAIN.
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CC -----
CC EMBL; M74532; -. NOT_ANNOTATED_CDS.
CC PROSITE; PS00893; MUTT; 1.
CC PRAM; PF00293; mutt; 1.
CC DOMAIN 124 157 MUTT-LIKE.
SQ SEQUENCE 260 AA; 30460 MW; C35DDF27 CRC32;

Query Match 6.5%; Score 104; DB 1; Length 260;
Best Local Similarity 30.2%; Pred. No. 2.47e-02;
Matches 16; Conservative 19; Mismatches 15; Indels 3; Gaps 3;

Db 147 EINIDSKDIYD-SRFVH-LFIEDLLSNRYVETILFLGNTLTSTNEILNNEL 197
QY 164 ESGVQSKNIYQNLQSLHLYQVNSTISVRV-DNFQYVDNTFPLDNLVLSVEL 215

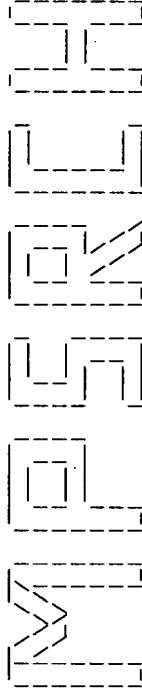
RESULT 9
ID FASL_RAT STANDARD; PRT; 278 AA.
AC P36940;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE FAS ANTIGEN LIGAND.
GN APTILG1 OR FASL.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94084792.
RA SUDA T., TAKAHASHI T., GOLSTEIN P., NAGATA S.;
RT "Molecular cloning and expression of the Fas ligand, a novel member
RT of the tumor necrosis factor family.";
RL CELL 75:1169-1178(1993).
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCE THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC KIDNEY AND LUNG.
CC -1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
CC EMBL; U03470; G440179; -.
CC PROSITE; PS00251; TNF_1; 1.
CC PRAM; PF00229; TNF; 1.
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CC	-----	
DR	EMBL; U19027; G609365; -	
DR	EMBL; D55634; G1871134; -	
DR	SGD; L0003514; TH17.	
DR	TRANSMEMBRANE; TRANSPORT.	
KW	TRANSMEMBRANE; TRANSPORT.	
FT	TRANSMEM 42	POTENTIAL.
FT	TRANSMEM 62	POTENTIAL.
FT	TRANSMEM 74	POTENTIAL.
FT	TRANSMEM 94	POTENTIAL.
FT	TRANSMEM 112	POTENTIAL.
FT	TRANSMEM 132	POTENTIAL.
FT	TRANSMEM 174	POTENTIAL.
FT	TRANSMEM 194	POTENTIAL.
FT	TRANSMEM 198	POTENTIAL.
FT	TRANSMEM 218	POTENTIAL.

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CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC
DR EMBL; U32744; G1573609; -
DR TIGR; H10615; -
DR PROSITE; PS00894; HTH_DEOR_FAMILY; 1.
DR PFAM; PF00455; deor; 1.
DR KX FUCOSE METABOLISM; TRANSCRIPTION REGULATION; ACTIVATOR;
KW DNA-BINDING. 18 37 H-T-H MOTIF (POTENTIAL).
FT DNA_BIND 249 AA; 28163 MW; 9ECE74A2 CRC32;
SQ SEQUENCE
. Query Match 6.2%; Score 99; DB 1; Length 249;
Best Local Similarity 19.6%; Pred. No. 1.33e-01;

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(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Aug 13 16:49:44 1999; MasPar time 15.65 Seconds
Tabular output not generated. 767.313 Million cell updates/sec

Title: >US-09-079-785-19
Description: (1-220) from US09079785.pep
Perfect Score: 1588
Sequence: 1 MQVQPGSVASPRWRPWS.....DTNTFPLDNVLSVFLYSSSD 220

Scoring table: PAM 150
Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrmb19

1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 44.383; Variance 83.620; scale 0.531

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1156	72.8	234	4	CD30L PROTEIN.	7.53e-221
2	114	7.2	279	11	FAS LIGAND.	3.60e-03
3	111	7.0	479	11	PHOSPHOPROTEIN PHOSPHA	9.85e-03
4	111	7.0	499	11	PROTEIN PHOSPHATASE 5.	9.85e-03
5	104	6.5	619	3	CHROMOSOME XV READING	9.68e-02
6	103	6.5	693	6	SODIUM-DEPENDENT PHOS	1.33e-01
7	103	6.5	2051	5	RECEPTOR TYROSINE PHOS	1.33e-01
8	100	6.3	249	4	TWEAK.	3.43e-01
9	100	6.3	332	10	RIBITOL DEHYDROGENASE	3.43e-01
10	100	6.3	492	13	PROTEIN PHOSPHATASE 5	3.43e-01
11	100	6.3	1010	5	F55C5.4 PROTEIN.	3.43e-01
12	96	6.0	414	5	SIMILARITY TO QUAIL NE	1.17e+00
13	95	6.0	419	5	CYCLIN A.	1.59e+00
14	95	6.0	445	10	HOMOLOG OF DTPD-GLUCOS	1.59e+00
15	95	6.0	594	2	PUTATIVE TRANSPORT PRO	1.59e+00
16	95	6.0	711	13	PROTEIN TYROSINE KINAS	1.59e+00
17	95	6.0	1153	3	JAK1 KINASE.	1.59e+00
18	96	6.0	4910	3	SIMILARITY NEAR N-TERM	1.17e+00
19	94	5.9	184	2	BC541A PROTEIN (FRAGME	2.14e+00
20	94	5.9	203	5	F26G5.3 PROTEIN.	2.14e+00

21	93	5.9	225	11	054907	TNF-RELATED WEAK INDUC	2.88e+00
22	94	5.9	434	10	064886	PUTATIVE HEME A:FARNES	2.14e+00
23	94	5.9	476	2	044636	TRANS-ACTING POSITIVE	2.14e+00
24	93	5.9	575	2	007570	HYPOTHETICAL 66.4 KD P	2.88e+00
25	93	5.9	863	14	041552	ENVELOPE GLYCOPROTEIN	2.88e+00
26	94	5.9	1099	5	020073	COSMID F35H10.	2.14e+00
27	94	5.9	1165	5	001923	SIMILARITY TO PROTEIN-	2.14e+00
28	94	5.9	1404	5	001363	CELF35-1.	2.14e+00
29	93	5.9	1564	6	028689	EPITHELIAL BASOLATELAR	2.88e+00
30	94	5.9	1581	5	045071	C11D2.6 PROTEIN.	2.14e+00
31	92	5.8	155	2	034694	YTAB PROTEIN.	3.87e+00
32	92	5.8	314	2	052264	3-METHYLCATECHOL 2,3-D	3.87e+00
33	92	5.8	524	5	077098	CYCLIN E.	3.87e+00
34	92	5.8	570	5	001501	SIMILAR TO CYCLIN.	3.87e+00
35	92	5.8	851	14	056110	ENVELOPE GLYCOPROTEIN.	3.87e+00
36	91	5.7	187	2	033557	AGRB.	5.19e+00
37	91	5.7	240	4	043557	TUMOR NECROSIS FACTOR	5.19e+00
38	91	5.7	240	4	075476	LIGAND FOR HERPESVIRUS	5.19e+00
39	91	5.7	330	3	014133	HYPOTHETICAL 38.0 KD P	5.19e+00
40	90	5.7	340	14	056873	HYPOTHETICAL 38.1 KD P	6.93e+00
41	91	5.7	412	3	008421	CHROMOSOME XV READING	5.19e+00
42	91	5.7	669	2	036151	P-AMINOBENZOIC ACID SY	5.19e+00
43	90	5.7	847	14	069996	ENVELOPE GLYCOPROTEIN	6.93e+00
44	90	5.7	854	14	069998	ENVELOPE GLYCOPROTEIN	6.93e+00
45	91	5.7	1524	1	054436	TETRABRACHION PRECURSO	5.19e+00

ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	234	AA.
AC	043404				
DT	01-JUN-1998	(TREMBREL. 06, CREATED)			
DT	01-JUN-1998	(TREMBREL. 06, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998	(TREMBREL. 08, LAST ANNOTATION UPDATE)			
DE	CD30L PROTEIN.				
GN	CD30L.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;				
OC	CATARRHINI; HOMINIDAE; HOMO.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 98007874.				
RA	CROAGER E.J.; ABRAHAM L.J.;				
RT	"Characterisation of the human CD30 ligand gene structure."				
RL	BIOCHIM. BIOPHYS. ACTA 1353:231-235(1997).				
DR	EMBL; AF006384; G2815515;				
DR	EMBL; AF006381; G2815515; JOINED.				
DR	EMBL; AF006382; G2815515; JOINED.				
DR	EMBL; AF006383; G2815515; JOINED.				
DR	PROSITE; PS00251; TNF-1; 1.				
SQ	SEQUENCE 234 AA; 25963 MW; B6137845 CRC32;				

Query Match	72.8%;	Score 1156;	DB 4;	Length 234;
Best Local Similarity	72.3%;	Pred. No. 7.53e-221;		
Matches	146;	Conservative 33;	Mismatches 22;	Indels 1; Gaps 1;
Db	33	TTSRSYFLTTATLALCIVFTVATIMVLVQRTDSIPNSPDNVPKLGKNCSEDLCLILKR	92	
Qy	20	STSRSYFLSTAL-VCLVAVAILVLVQKDKSTPTNTEKAPKLGKNCSEDLCLILKR	78	
Db	93	APFKSWAYLQVAKHLNKLKSNKDGILHGVRYODGNLVQFPGLYFIICQLFVQCP	152	
Qy	79	TPSKSWAYLQVSKHLNKLKSNWEDGTHGLIYQDGNLVQFPGLYFIICQLFVQCS	138	
Db	153	NNSYDLKXELLINKHKKQLVTVCESCMQTKHYQNLQSLDLYQVNTTISVNDYQ	212	
Qy	139	NHSVDLTLQLLNKIKKQTLTVTVCESGVQSKNIYQNLQSLDLYQVNTTISVNDYQ	198	
Db	213	YDITSTFPLENVLSIFLKNSD	234	
Qy	199	YVDINTFPLDNVLSVFLYSSD	220	

[illegible]

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AC Q04308;
AD 01-JUN-1998 (TREMUREL. 06, CREATED)
DT 01-JUN-1998 (TREMUREL. 06, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMUREL. 08, LAST ANNOTATION UPDATE)
DE TWEAK.
DN APO3L.
GN HOMO SAPIENS (HUMAN).
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
NC [1]
RC SEQUENCE FROM N.A.
RC TISSUE-TONSIL;
RX MEDLINE; 98070415.
RA CHICHEPORTICHE Y., BOURDON P.R., XU H., HSU Y.-M., SCOTT H., HESSON C., GARCIA I., BROWNING J.L.;
RT "TWEAK, a new secreted ligand in the tumor necrosis factor family that weakly induces apoptosis.";
RL J. BIOL. CHEM. 272:32401-32410(1997).
RN [2]
RP SEQUENCE FROM N.A.
RP MEDLINE; 98228355.
RX MARSTERS S.A., SHERIDAN J.P., PITTI R.M., BRUSH J., GODDARD A., ASHKENAZI A.;
RT "Identification of a ligand for the death-domain-containing receptor Apo3."
RL CURR. BIOL. 8:525-528(1998).
DR EMBL; AF030099; G2707219; -.
DR EMBL; AF055872; G3108231; -.
SQ SEQUENCE 249 AA; 27216 MW; 3AEC1F1 CRC32;

Query Match      6.3%; Score 100; DB 4; Length 249;
Best Local Similarity 37.5%; Pred. No. 3.43e-01;
Matches 15; Conservative 15; Mismatches 7; Indels 3; Gaps 3

Db 149 OIGEFIVTRAGLYLCQVHF-DE-GK-AVYKLKLLVDG 185
| :||::| :||::| :||::| :||::| :||::| :||::| :||::| :||::| :||::|
QY 113 ODGNLIYVFPGLYFIVCOLOPLVCQSNHSVDLTQLLINS 152

RESULT 9
ID Q02985 PRELIMINARY; PRT; 332 AA.
AC Q02985;
AD 01-JAN-1998 (TREMUREL. 05, CREATED)
DT 01-JAN-1998 (TREMUREL. 05, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMUREL. 08, LAST ANNOTATION UPDATE)
DE RIBITOL DEHYDROGENASE ISOLOG.
GN T19F06.14.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OS EUKARYOTA; VIRIDIPLANETAE; STREPTOPHYTA; EMERYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE; CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLOMBIA;
RA ROUSLEYS T.A., LIN X., KETCHUM K.A., CROSSBY M.L., BRANDON R.C., SPRINGS T.A., MASON T.M., KERLAVAGE A.R., ADAMS M.D., SOMERVILLE C.R., VENTER J.C.;
RL SUBMITTED (JUL-1997) TO ENBL/GENBANK/DBDJ DATA BANKS.
DR EMBL; AC002343; G2262111; -.
DR FRAM; PF00106; adh_short; 1.
SQ SEQUENCE 332 AA; 35840 MW; A4E08F03 CRC32;

Query Match      6.3%; Score 100; DB 10; Length 332;
Best Local Similarity 36.0%; Pred. No. 3.43e-01;
Matches 18; Conservative 9; Mismatches 23; Indels 0; Gaps 0

Db 109 SLDFPLNLLINNACKLAHEHAISEDGIEMTFATNYLGHLTNLLNKMI 158
|:||| ||||| | :||::| :||::| :||::| :||::| :||::| :||::| :||::|
QY 141 SVDLTLQLLNKKIKQTFLTVCSGVQSNNYQNLSQFLHLHYLVNSTI 190

RESULT 10
ID Q04205 PRELIMINARY; PRT; 492 AA.

```



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O42205;
AC 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PROTEIN PHOSPHATASE 5 (FRAGMENT).
GN PP5.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RA OLENDORFF V., DONOGHUE D.J.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF018263; G2407639; -.
DR PFAM; PF00149; Stposphatase; 1.
DR PFAM; PF00515; TPR; 2.
FT NON_TER
FT 1
SQ SEQUENCE 492 AA; 56144 MW; C503341E CRC32;

Query Match 6.3%; Score 100; DB 13; Length 492;
Best Local Similarity 22.7%; Pred. No. 3.43e-01;
Matches 20; Conservative 28; Mismatches 34; Indels 6; Gaps 6;

Db 201 CUYQMLVQVKD-ILS-KLPSLVEVSLEKSOQVTVCGDTHGQ-FYDLNIFHLNGLPSN 256
QY 129 COLQFLVQCSNHSVDLTQLLNSKIKKQTLVTVCSGVQSKNIYQNLQFLHYLVQNS 188

Db 257 NPYI-FNG-DFVDRGSFSVEVITLFGF 282
QY 189 TISVRVDFNQYVDTNFTPLDNLVSLVELY 216

RESULT 11
ID Q20818 PRELIMINARY; PRT; 1010 AA.
AC Q20818;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE F55C5.4 PROTEIN.
DE F55C5.4.
GN F55C5.4.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTERA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RA HARRIS B.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).

RESULT 12
ID P91486 PRELIMINARY; PRT; 414 AA.
AC P91486;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SIMILARITY TO QUAIL NEURONAL CELL CYCLE WITHDRAWAL PROTEIN.
GN T21E12.2.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTERA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).

RESULT 13
ID O77212 PRELIMINARY; PRT; 419 AA.
AC O77212;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CYCLIN A.
OS DREISSENA POLYMORPHA (ZEBRA MUSSEL).
OC EUKARYOTA; METAZOA; MOLLUSCA; BIVALVIA; HETEROCONCHIA; VENEROIDA;
OC DREISSENIDAE; DREISSENA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA LAMERS A.E., HEINEY J., RAM J.L.;
RT "Cloning and sequence analysis of two cDNAs encoding cyclin A and
RT cyclin B in the zebra mussel Dreissena polymorpha.";
RT SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
```

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Db 297 ACUTAPEYG 305
QY 209 NVLSVFLYS 217

RESULT 12
ID P91486 PRELIMINARY; PRT; 414 AA.
AC P91486;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SIMILARITY TO QUAIL NEURONAL CELL CYCLE WITHDRAWAL PROTEIN.
GN T21E12.2.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTERA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).

RESULT 13
ID O77212 PRELIMINARY; PRT; 419 AA.
AC O77212;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CYCLIN A.
OS DREISSENA POLYMORPHA (ZEBRA MUSSEL).
OC EUKARYOTA; METAZOA; MOLLUSCA; BIVALVIA; HETEROCONCHIA; VENEROIDA;
OC DREISSENIDAE; DREISSENA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA LAMERS A.E., HEINEY J., RAM J.L.;
RT "Cloning and sequence analysis of two cDNAs encoding cyclin A and
RT cyclin B in the zebra mussel Dreissena polymorpha.";
RT SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
```

RESULT	15	
ID	O30425	PRELIMINARY; PRT; 594 AA.
AC	O30425;	
DT	01-JAN-1998	(TREMBREL. 05, CREATED)
DT	01-JAN-1998	(TREMBREL. 05, LAST SEQUENCE UPDATE)
DT	01-NOV-1998	(TREMBREL. 08, LAST ANNOTATION UPDATE)
DE	PUTATIVE TRANSPORT PROTEIN (XING), PUTATIVE TRANSPORT PROTEIN	
DE	(XYNH), XYLANASE (XYNF), XYLANASE (XYNE), XYLANASE (XYND), XYLANASE	
DE	(XYNA), ACETILXYLOSIDASE (XYNC) AND XYLANASE	
DE	(XYNB) GENES, COMPLETE CDS (XYNH) (XYNE) (XYNA) (XYNC) (XYNB).	
OC	CALDICELLULOSITRUCTOR SACCHAROLYTICUS.	
OC	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;	
OC	THERMOANAEROBACTER GROUP; CALDICELLULOSITRUCTOR.	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RP	MEDLINE; 90253140.	
RX	LUTHI E., LOVE D.R., MCANULTY J., WALLACE C., CAUGHEY P.A., SAUL D.,	
RA	BERGQUIST P.L.;	
RA	"Cloning, sequence analysis, and expression of genes encoding	
RT	xylan-degrading enzymes from the thermophile "Caldocellum	
RT	saccharolyticum".;	
RL	APPL. ENVIRON. MICROBIOL. 56:1017-1024(1990).	
RN	[2]	
RN	SEQUENCE FROM N.A.	

W P S R L

(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Aug 13 16:51:07 1999; MasPar time 10.12 Seconds
Tabular output not generated. 451.764 Million cell updates/sec

Title: >US-09-079-785-23
Description: (1-215) from US09079785.pep
Perfect Score: 1566
Sequence: 1 MHVPAGSVASHLGTTSRYF.....DSTFPLENVLISFLYSNSD 215

Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 32.216; Variance 154.370; scale 0.209

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1566	100.0	215	8 R45007	Sequence encoded by a	1.15e-125
2	1566	100.0	234	8 R45009	Sequence encoded by a	1.15e-125
3	1189	75.9	220	8 R45006	Sequence encoded by a	3.53e-92
4	1189	75.9	239	8 R45008	Sequence encoded by a	3.53e-92
5	118	7.5	154	3 P50502	Human tumour necrosis	9.43e-01
6	118	7.5	180	23 W10875	FasL/IT-alpha hybrid.	9.43e-01
7	115	7.3	137	14 R79067	Mouse Fas ligand (par	1.53e+00
8	115	7.3	137	14 R79068	Mouse Fas ligand (par	1.53e+00
9	115	7.3	157	23 W10877	TNFI/IT-alpha hybrid.	1.53e+00
10	115	7.3	157	12 R62470	Tumour necrosis facto	1.53e+00
11	115	7.3	179	14 R79069	Mouse Fas ligand (par	1.53e+00
12	114	7.3	216	38 W68412	Hybrid alpha-1-thymos	1.80e+00
13	115	7.3	279	18 R68357	Mouse Fas ligand.	1.53e+00
14	115	7.3	279	14 R77282	Mouse Fas-l. protein.	1.53e+00
15	115	7.3	279	14 R79098	Mouse Fas ligand.	1.53e+00
16	113	7.2	151	1 P81233	Anti-tumour peptide.	2.12e+00

17	112	7.2	154	11 R69578	Human TNF mutein.	2.48e+00
18	111	7.1	130	14 R79096	Human Fas ligand C-te	2.91e+00
19	111	7.1	136	33 W48955	Fas ligand fragment (2.91e+00
20	111	7.1	136	14 R8307	N-terminally deleted	2.91e+00
21	111	7.1	137	14 R79100	Human Fas ligand (par	2.91e+00
22	111	7.1	137	14 R8306	N-terminally deleted	2.91e+00
23	111	7.1	138	14 R8305	N-terminally deleted	2.91e+00
24	111	7.1	138	14 R79064	Human Fas ligand (par	2.91e+00
25	111	7.1	139	14 R8304	N-terminally deleted	2.91e+00
26	111	7.1	141	14 R8303	N-terminally deleted	2.91e+00
27	111	7.1	145	27 W35848	Human FAS-ligand for	2.91e+00
28	111	7.1	151	26 W16667	Human Fas ligand (hfa	2.91e+00
29	111	7.1	158	4 R22723	TNF polypeptide mutei	2.91e+00
30	111	7.1	178	14 R8308	C-terminally deleted	2.91e+00
31	111	7.1	179	14 R79099	Human Fas ligand (par	2.91e+00
32	111	7.1	179	23 W11814	Fas ligand.	2.91e+00
33	111	7.1	265	33 W48954	Non-cleavable Fas lig	2.91e+00
34	111	7.1	268	33 W48953	Non-cleavable Fas lig	2.91e+00
35	111	7.1	281	14 R77281	Human Fas-L protein.	2.91e+00
36	111	7.1	281	36 W75959	Human Fas ligand.	2.91e+00
37	111	7.1	281	14 R79097	Human Fas ligand.	2.91e+00
38	111	7.1	281	18 R8356	Human Fas ligand.	2.91e+00
39	111	7.1	281	35 W49105	Fas Ligand.	2.91e+00
40	111	7.1	281	18 R98104	Human Fas ligand deri	2.91e+00
41	111	7.1	281	26 W27143	Human Fas ligand.	2.91e+00
42	111	7.1	287	26 W27146	CH3/Fas ligand domain	2.91e+00
43	111	7.1	378	27 W35864	Human FAS-ligand:tgG2	2.91e+00
44	110	7.0	150	1 P81066	Sequence of new physi	3.42e+00
45	110	7.0	161	4 R22308	TNF polypeptide mutei	3.42e+00

ALIGNMENTS

RESULT	1
ID	R45007 standard; Protein; 215 AA.
AC	R45007;
DT	19-JUN-1994 (first entry)
DE	Sequence encoded by a human CD30-L cDNA clone.
KW	Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW	CD30 ligand; CD30-L; TNF; NGF.
OS	Homo sapiens.
FT	Key Location/Qualifiers
FT	region 22..43
FT	/label= transmembrane
FN	W09324135-A.
PD	09-DEC-1993.
PF	25-MAY-1993; U04926.
PR	26-MAY-1992; US-889717.
PR	02-JUN-1992; US-892459.
PR	15-JUN-1992; US-899660.
PR	01-JUL-1992; US-907224.
PR	27-OCT-1992; US-966775.
PA	(IMMUNEX) IMMUNEX CORP.
PI	Armitage RJ, Goodwin RG, Smith CA;
DR	WPI: 93-405417/50.
DR	N-PSDB; Q53536.
PT	New cytokine, CD30-L, which binds CD30 - used for developing
PT	prods. for diagnosis, detection, purifications, research and
PT	therapy
PS	Claim 15; Figure 5a; 59pp; English.
CC	CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC	as a clinical marker for Hodgkin's lymphoma and related haematologic
CC	malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC	L and other derived prods. can be used for elucidating the roles
CC	that CD30 and CD30-L may play in the immune system and for diagnosis
CC	and therapy. It can be isolated as follows. A cDNA library prepd. from
CC	the murine Heiler T-cell line 7B9 is screened with a CD30/FC fusion
CC	protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
CC	This cDNA can then be used as a probe to screen a human PBL cDNA
CC	library to obtain cDNA encoding human CD30-L.
SQ	Sequence 215 AA;
Query Match	100.0%; Score 1566; DB 8; Length 215;

PS Disclosure; Fig 10; 87pp; English.

CC This sequence comprises the C-terminal extracellular domain of the Fas
CC ligand altered to drive trimerisation with wild-type lymphotoxin (LT)-
CC beta. LT subunit association domains potentiate subunit associations into
CC an active trimeric ligand. Tumour necrosis factor (TNF)-related ligand
CC monomers mutated in their respective subunit associations domains can
CC form heteromeric complexes with LT subunits. LT-alpha/beta heteromeric
CC complexes and LT heterotrimeric complexes are useful as inhibitors of
CC signalling by TNF receptors (R) and TNF-related receptors, such as CD40,
CC Fas and LT-beta receptors. By inhibiting TNF-R signalling the complexes
CC (esp., LT-alpha2/beta1) can be used for treating autoimmune diseases
CC including diabetes, rheumatoid arthritis, inflammatory bowel disease and
CC HIV proliferation, known to be improved by TNF inhibition. The complexes
CC are also useful for preventing or reducing the severity of an immune
CC response to a tissue graft.
SQ Sequence 180 AA;

Query Match 7.5%; Score 118; DB 23; Length 180;

Best Local Similarity 31.4%; Pred. No. 9.43e-01;

Matches 27; Conservative 19; Mismatches 33; Indels 7; Gaps 6;

Db 41 lrka-ahl-tgknsrsmplewedygvlxgvykkgglvinetglyfvsxvfrq 98

QY 76 FKRSWAYLOVAKHLNKT-KLSWKKD-GI--LHGVRQDGNLVIOFPGLYFIICQLQFLVQ 131

Db 99 scnnplshkvymrnsqpqdlvils 124

QY 132 -CPNNSVDLKLLELLINKHKKQALVT 156

RESULT 7

ID R79067 standard; Protein; 137 AA.

AC R79067;

DT 22-FEB-1996 (first entry)

DE Mouse Fas ligand (partial sequence).

KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;

KW Fas cell surface antigen; Fas-L; mouse.

OS Mus musculus.

PN W09513293-A1.

PD 18-MAY-1995.

PF 10-NOV-1994; J01899.

PR 10-NOV-1993; JP-305975.

PR 13-DEC-1993; JP-342526.

PR 18-MAR-1994; JP-074344.

PR 08-JUL-1994; JP-180955.

PR 07-SEP-1994; JP-239363.

PR 18-OCT-1994; JP-278378.

PA (MOCH) MOCHIDA PHARM CO LTD.

PA (OSAB-) OSAKA BIOSCIENCE INST.

PI Nagata S, Nakamura N, Suda T, Takahashi T;

DR WPI; 95-194031/25.

DR N-PSDB; Q99496.

PT Peptide which binds to Fas antigen, and antibody reactive with it -
PT for treatment and diagnosis of viral or auto:immune diseases

PS Claim 9; Page 219-221; 300pp; Japanese.

CC Fas ligands or active fragments able to induce apoptosis in cells

CC which express the Fas cell surface antigen are claimed. The

CC proteins are isolated from human, rat and mouse sources. The present

CC sequence represents part of the mouse Fas ligand.

SQ Sequence 137 AA;

Query Match 7.3%; Score 115; DB 14; Length 137;

Best Local Similarity 35.4%; Pred. No. 1.53e+00;

Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 3 ahltnphrsrplewedygtaligvykkgglvinetglyfvsxvfrqscnnp 62

QY 81 AYLOVAKHLNKTLSWKKD-GI-L-HGVRQDGNLVIOFPGLYFIICQLQFLVQ-CPNNS 136

Db 63 lnhkv 67

QY 137 VDLKL 141

RESULT 8

ID R79068 standard; Protein; 138 AA.

AC R79068;

DT 22-FEB-1996 (first entry)

DE Mouse Fas ligand (partial sequence).

KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;

KW Fas cell surface antigen; Fas-L; mouse.

OS Mus musculus.

PN W09513293-A1.

PD 18-MAY-1995.

PF 10-NOV-1994; J01899.

PR 10-NOV-1993; JP-305975.

PR 13-DEC-1993; JP-342526.

PR 18-MAR-1994; JP-074344.

PR 08-JUL-1994; JP-180955.

PR 07-SEP-1994; JP-239363.

PR 18-OCT-1994; JP-278378.

PA (MOCH) MOCHIDA PHARM CO LTD.

PA (OSAB-) OSAKA BIOSCIENCE INST.

PI Nagata S, Nakamura N, Suda T, Takahashi T;

DR WPI; 95-194031/25.

DR N-PSDB; Q99497.

PT Peptide which binds to Fas antigen, and antibody reactive with it -
PT for treatment and diagnosis of viral or auto:immune diseases

PS Claim 10; Page 221-222; 300pp; Japanese.

CC Fas ligands or active fragments able to induce apoptosis in cells

CC which express the Fas cell surface antigen are claimed. The

CC proteins are isolated from human, rat and mouse sources. The present

CC sequence represents part of the mouse Fas ligand.

SQ Sequence 138 AA;

Query Match 7.3%; Score 115; DB 14; Length 138;

Best Local Similarity 35.4%; Pred. No. 1.53e+00;

Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 4 ahltnphrsrplewedygtaligvykkgglvinetglyfvsxvfrqscnnp 63

QY 81 AYLOVAKHLNKTLSWKKD-GI-L-HGVRQDGNLVIOFPGLYFIICQLQFLVQ-CPNNS 136

Db 64 lnhkv 68

QY 137 VDLKL 141

RESULT 9

ID W10877 standard; Protein; 157 AA.

AC W10877;

DT 25-SEP-1997 (first entry)

DE TNFL/LT-alpha hybrid.

KW C-terminal extracellular domain; CD40 ligand; mutated; trimerisation;

KW lymphotoxin; LT; beta; alpha; tumour necrosis factor; TNF; inhibitor;

KW signalling; receptor; Fas; treating; autoimmune disease; diabetes;

KW rheumatoid arthritis; inflammatory bowel disease; HIV proliferation;

KW immune response; tissue graft.

OS Synthetic.

PH Key Location/Qualifiers

FT misc_difference 13

FT /note= "LT-alpha subunit association domain residue"

FT misc_difference 36..38

FT /note= "LT-alpha subunit association domain residues"

FT misc_difference 38

FT /note= "given as O in the specification"

FT misc_difference 57..58

FT /note= "LT-alpha subunit association domain residues"

FT misc_difference 63

FT /note= "LT-alpha subunit association domain residue"

FT misc_difference 95..98

FT /note= "LT-alpha subunit association domain residues"

FT misc_difference 97

FT /note= "given as O in the specification"

FT misc_difference 116..117

FT /note= "LT-alpha subunit association domain residues"

FT misc_difference 121..123
FT /note= "LT-alpha subunit association domain residues"
FT misc_difference 148
FT /note= "LT-alpha subunit association domain residue"
FT misc_difference 150
FT /note= "LT-alpha subunit association domain residue"
FT misc_difference 154..155
FT /note= "LT-alpha subunit association domain residues"
FT W09640774-A1.
PN PD 19-DEC-1996.
PD PF 06-JUN-1996: U09773.
PR 07-JUN-1995: US-476074.
PA (BIOJ) BIOGEN INC.
PI Browning JL, Karpusas MN, Meier W;
WPI: 97-087055/08.
DR Heteromeric complexes comprising lymphotoxin sub-units - useful as
PT inhibitors of signalling by TNF- and TNF-related receptors, for
PT treating auto-immune disease, graft rejection. etc.
PT Disclosure: Fig 10: 87pp: English.
PS This sequence comprises the C-terminal extracellular domain of the TNF
CC ligand altered to drive trimerisation with wild-type lymphotoxin (LT)-
CC beta. LT subunit association domains potentiate subunit associations into
CC an active trimeric ligand. Tumour necrosis factor (TNF)-related ligand
CC monomers mutated in their respective subunit associations domains can
CC form heteromeric complexes with LT subunits. LT-alpha/beta heteromeric
CC complexes and LT heterotrimeric complexes are useful as inhibitors of
CC signalling by TNF receptors (R) and TNF-related receptors, such as CD40,
CC FAS and LT-beta receptors. By inhibiting TNF-R signalling the complexes
CC (esp. LT-alpha2/beta1) can be used for treating autoimmune diseases
CC including diabetes, rheumatoid arthritis, inflammatory bowel disease and
CC HIV proliferation, known to be improved by TNF inhibition. The complexes
CC are also useful for preventing or reducing the severity of an immune
CC response to a tissue graft.
SO Sequence 157 AA:

```

Query Match      7.3%; Score 115; DB 23; Length 157;
Best Local Similarity 36.1%; Pred. No. 1.53e+00;
Matches 26; Conservative 14; Mismatches 26; Indels 6; Gaps 5;

Db      6 rtpsdkpaahv-vanpqaeqqlqwlrranafingvvelrdqlvpsseglyfvsqvlf 64
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      73 RAPFKKSMAYLQVAKHLNKTLSW-NK--DGIL-HGVRYPQGNLVIOFPGLYFICQLQF 128
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db      65 kgqgcpcsthvll 76
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      129 LVO-CPNNSVDL 139

RESULT      10
ID      R62470 standard; Protein; 157 AA.
AC      R62470;
DE      05-JUN-1995 (first entry)
DE      Tumour necrosis factor-alpha mutem L75H.
KW      Human; tumour necrosis factor; TNF; TNF-a; expression; mutein; mutation;
KW      receptor; affinity; therapeutic; diagnostic; cancer therapy; cancer;
KW      obesity; septic shock; meningitis.
OS      Synthetic.
FH      Key
FT      Location/Qualifiers
FT      misc_difference 75
FT      /label= Leu to His
FT      EP-619372-A.
PD      12-OCT-1994.
PF      17-MAR-1994; 104154.
PR      29-MAR-1993; EP-810224.
PA      (HOFF) HOFFMANN LA ROCHE & CO AG F.
PI      Banner D, Lesslauer W, Lotscher H, Stuber D, Loetscher H;
PI      Stueber, D;
DR      WPI; 94-311810/39.
DR      N-PSDB: Q87689.
PT      New human TNF-a muteins with higher affinity for p75-TNFR -
PT      useful e.g. for cancer therapy, treatment of obesity and toxic
PT      shock.
PS      Claim 4; Page 15; 53pp; English.

```

CC The amino acid sequence of the mutated human tumour necrosis factor alpha (TNF-a). The mutant differs from the wild type at position 75 with a change from a Leu residue to a His residue. The gene encoding the protein is placed in the expression plasmid pDS56/RBSII and called pDS56/RBSII.SphI-TNFa(L75H). The expression of the wild type or mutant proteins is regulated by the lac repressor present on the plasmid PREP4. The gene encoding the protein is mutated at specific sites resulting in a series of mutated proteins (R62464-83 and R63093-103). The biological activities of TNF are mediated via specific receptors of mol. wt. 55 and 75 kDa called p55-TNF-R and p75-TNF-R respectively. The mutated proteins presented have a higher affinity for the human p75-TNF receptor than for the p55-TNF receptor. The mutated proteins can be used in a variety of therapeutic or diagnostic applications including cancer therapy, treatment of obesity, septic shock or bacterial meningitis. Sequence 157 AA;

Query Match 7.3%; Score 115; DB 12; Length 157;
Best Local Similarity 36.1%; Pred. No. 1.53e+00;
Matches 26; Conservative 14; Mismatches 26; Indels 6; Gaps 5;

Db 6 rtpeckpvahv-vanpqaegqlwnrranallangvelrdnqlvypseglyliysqvlv 64
QY 73 RAFPKKSWAYLQVAHKLNLTKLSW-NK--DGIIL-HGVRYQGNLVLPFGLYIICQLQF 128
Db 65 kggcgpcsthvhl 76
QY 129 LVQ-CPNNSVDL 139

RESULT 11
ID IC R79069 standard; Protein; 179 AA.
AC R79069;
DT 22-FEB-1996 (first entry)
DE Mouse Fas ligand (partial sequence).
KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; Fas-L; mouse.
PN Mus musculus.
PN WQ9513293-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; J01899.
PR 10-NOV-1993; JP-305975.
PR 13-DEC-1993; JP-342526.
PR 18-MAR-1994; JP-074344.
PR 08-JUL-1994; JP-180955.
PR 07-SEP-1994; JP-239363.
PR 18-OCT-1994; JP-278378.
PA (MOCH) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
PI Nagata S, Nakamura N, Suda T, Takahashi T;
DR WPI; 95-194031/25.
DR N-PSDB; Q99498.
PT Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto-immune diseases
PS Claim 11; Page 222-224; 300pp; Japanese.
CC Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the mouse Fas ligand.
SQ Sequence 179 AA;

```
Query Match          7.3%; Score 115; DB 14; Length 179;
Best Local Similarity 35.4%; Pred. No. 1.53e+00;
Matches            8; Mismatches 30; Indels   4; Gaps   4;
```

Db 45 ahltnpharsipIewedytgatIsgrkykkgglvlnetgIyfyyskvyrfgscnnqp 104

QY 81 AYIQVAKHLNKTLSNKND-GI-L-HGVRYQDGNLVYIFPGLYFIICQLQFLVQ-CPNNS 136

Db 105 lnhkv 109

QY 137 VDLKL 141

```

RESULT 12
ID W68412 standard; Protein; 216 AA.
AC W68412;
DT 02-MAR-1999 (first entry)
DE Hybrid alpha-1-thymosin/tumour necrosis factor protein.
KW Hybrid; alpha-1-thymosin; tumour necrosis factor; immunostimulatory;
KW infectious disease.
OS Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 187
FT /label= unknown
FT /note= "given in specification as Fsp"
FT Misc_difference 207
FT /label= unknown
FT /note= "given in specification as Lus"
FT
FT
PN RU2102988-Cl.
PD 27-JAN-1998.
PF 27-JAN-1998.
PR 10-FEB-1995; 101728.
PR 10-FEB-1995; RU-101728.
PA (ZINC/) ZINCENKO E V.
PI Panin AN, Zinchenko EV, Zinchenko VB;
PI WPI; 98-454925/39.
DR Composition with immuno-stimulating properties - contains a hybrid
PT protein alpha-1-thymosin, a tumour necrosis factor
PS Example 1: Column 5-6; 10pp; Russian.
CC This sequence represents a hybrid protein comprising the alpha-1-thymosin
CC fused to the tumour necrosis factor. The protein is especially expressed
CC and purified from a microorganism (e.g. E. coli) transformed with the
CC plasmid phry325 containing the hybrid protein coding sequence. The hybrid
CC protein is used in immunostimulatory compositions for use in the
CC non-specific prevention and treatment of infectious diseases.
SQ Sequence 216 AA;

Query Match 7.3%; Score 114; DB 38; Length 216;
Best Local Similarity 36.1%; Pred. NO. 1.80e+00;
Matches 26; Conservative 15; Mismatches 25; Indels 6; Gaps 5;

Db 34 rtpsdkpvhv-vanpqagqqlqlrranallangvelrdnqlvvpseglyliysqvlf 92
  11: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 73 RAPFKKSNAYLQVAKHLNKTLSW-NK--DGIL-HGVRQDGNLVIOFPGLYFIICQLQF 128
  11: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 93 vgecpsthvll 104
  11: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 129 LVO-CPNNSVDL 139

RESULT 13
ID R88357 standard; Protein; 279 AA.
AC R88357;
DT 15-OCT-1995 (first entry)
DE Mouse Fas ligand.
KW Fas ligand; transplant rejection; autoimmune disease; diabetes;
KW inflammation; graft rejection; rheumatoid arthritis; allergy;
KW cystic fibrosis; multiple sclerosis.
OS Mus musculus.
FH Key Location/Qualifiers
FT peptide 101..279
FT /label= soluble mouse Fas ligand
FT
FT
PN W09532627-A1.
PD 07-DEC-1995.
PF 26-MAY-1995; U06742.
PR 27-MAY-1994; US-250478.
PR 26-JAN-1995; US-378507.
PA (COLS ) UNIV COLORADO.
PI Belligra D, Duke RC;
DR WPI; 96-030252/03.
DR N-PSDB; T09678.
PT use of Fas ligand - for suppressing lymphocyte-mediated immune
PT responses, e.g. transplant rejection or auto-immune conditions
PS Claim 6; Fig.1; 51pp; English.
CC The expressed protein can be used to suppress and prevent
CC T-lymphocyte-mediated transplant or graft rejection, T-lymphocyte-

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CC mediated disease recurrence or to treat T-lymphocyte-mediated
CC diseases. It can be used to treat diabetes, rheumatoid arthritis,
CC multiple sclerosis, cystic fibrosis or allergies.
SQ Sequence 279 AA;

Query Match 7.3%; Score 115; DB 18; Length 279;
Best Local Similarity 35.4%; Pred. NO. 1.53e+00;
Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 145 ahltnphrsrslpewedygtalisgvykkgglvlnetgylfvyksvfyrgscnnqp 204
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QY 81 AYLOVAKHLNKTLSW-NK-GI-L-HGVRQDGNLVIOFPGLYFIICQLQFLVQ-CPNNS 136
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Db 205 lnbkv 209
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QY 137 VDLKL 141

RESULT 14
ID R77282 standard; Protein; 279 AA.
AC R77282;
DT 05-DEC-1995 (first entry)
DE Mouse Fas-L protein.
KW Fas ligand; Fas-L; cell surface protein; autoimmune disease;
KW self-tolerance.
OS Mus sp.
FH Key Location/Qualifiers
FT domain 1..78
FT /label= Cytoplasmic_domain
FT domain 79..103
FT /label= Transmembrane_domain
FT domain 104..279
FT /label= Extracellular_domain
FT
PN W09518819-A.
PD 13-JUL-1995.
PF 06-JAN-1995; U00362.
PR 07-JAN-1994; US-179138.
PR 01-FEB-1994; US-190559.
PA (IMMV ) IMMUNEX CORP.
PI Goodwin RG;
PI WPI; 95-255032/33.
DR N-PSDB; Q91312.
PT Human and murine DNA encoding ligand(s) binding to cell surface protein
PT Fas - useful for studying auto-immune disorder(s) and development of
PT self-tolerance.
PS Disclosure; Page 29-30; 38pp; English.
CC A cDNA library prepd. from mouse peripheral blood lymphocyte mRNA was
CC screened with a murine Fas-L probe from the 3' end of Fas-L DNA.
CC An isolated clone (Q91312) encoded mouse Fas-L.
SQ Sequence 279 AA;

Query Match 7.3%; Score 115; DB 14; Length 279;
Best Local Similarity 35.4%; Pred. NO. 1.53e+00;
Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 145 ahltnphrsrslpewedygtalisgvykkgglvlnetgylfvyksvfyrgscnnqp 204
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QY 81 AYLOVAKHLNKTLSW-NK-GI-L-HGVRQDGNLVIOFPGLYFIICQLQFLVQ-CPNNS 136
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Db 205 lnbkv 209
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QY 137 VDLKL 141

RESULT 15
ID R79098 standard; Protein; 279 AA.
AC R79098;
DT 21-FEB-1996 (first entry)
DE Mouse Fas ligand.
KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; Fas-L; mouse.
OS Mus musculus.
FH Key Location/Qualifiers

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FT region 25..78 /label= proline-rich
FT FT /label= proline-rich
FT domain 79..100 /label= transmembrane_anchor
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FT modified_site 248
FT FT /label= N-glycosylation_site
FT modified_site 258
FT FT /label= N-glycosylation_site
FT WO9513293-A1
FT 18-MAY-1995
PD
PF 10-NOV-1994; J01899
PR 10-NOV-1993; JP-305975
PR 13-DEC-1993; JP-342526
PR 18-MAR-1994; JP-074344
PR 08-JUL-1994; JP-180955
PR 07-SEP-1994; JP-239363
PR 18-OCT-1994; JP-278378
PR (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
PI Nagata S, Nakamura N, Suda T, Takahashi T;
DR WPI; 95-194031/25
DR N-PSDB; Q94156, Q99499
PT Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto:immune diseases
PS Claim 12; Fig 23-24; 300pp; Japanese.
CC A clone (Q94156) contg. an insert coding for the mouse Fas ligand
CC was isolated using probes derived from a rat Fas-L clone (see
CC Q94153). The mouse sequence contains an open reading frame coding
CC for a 279 amino acid sequence with 5 N-glycosylation sites and a
CC proline-rich region. The deduced mouse amino acid sequence has
CC 91.4% homology with rat Fas-L. Fas ligands are able to induce
CC apoptosis in cells which express the Fas cell surface antigen.
SQ Sequence 279 AA;

Query Match 7.3%; Score 115; DB 14; Length 279;
Best Local Similarity 35.4%; Pred. No. 1.53e+00;
Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 145 ahltnphrsrslplewedygtaligvkykkgglvinetglyfvykvyfrgscnnqp 204
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 81 AYLQVAKHLNKRKLSWNKD-GI-L-HGVRYQDGNLVIOFFGLYFIICQLQFLVQ-CPNNS 136
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 205 lnhkv 209
: : | :
QY 137 VDLKL 141

Search completed: Fri Aug 13 16:51:51 1999
Job time : 44 secs.
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WILEY

(TM)

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Distribution rights by Oxford Molecular Ltd

MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:54:20 1999; Maspar time 3.71 Seconds
Tabular output not generated. 587.716 Million cell updates/sec

Title: >US-09-079-785-23
Description: (1-215) from US09079785.pep
Perfect Score: 1566
Sequence: 1 MHVPAGSVASHLGTTSRSVF.....DSTFPLENVLSIFLYNSD 215

Scoring table: PAM 150
Gap 11

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 30.077; Variance 145.438; scale 0.207

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1566	100.0	215	1	US-08-570- Sequence 23, Applicati	1.76e-125
2	1566	100.0	215	2	US-08-580- Sequence 23, Applicati	1.76e-125
3	1566	100.0	215	1	US-08-225- Sequence 23, Applicati	1.76e-125
4	1566	100.0	234	1	US-08-570- Sequence 8, Applicatio	1.76e-125
5	1566	100.0	234	2	US-08-580- Sequence 8, Applicatio	1.76e-125
6	1566	100.0	234	1	US-08-225- Sequence 8, Applicatio	1.76e-125
7	1189	75.9	220	1	US-08-570- Sequence 19, Applicati	3.04e-92
8	1189	75.9	220	1	US-08-225- Sequence 19, Applicati	3.04e-92
9	1189	75.9	220	2	US-08-580- Sequence 19, Applicati	3.04e-92
10	1189	75.9	239	1	US-08-570- Sequence 6, Applicatio	3.04e-92
11	1189	75.9	239	2	US-08-580- Sequence 6, Applicatio	3.04e-92
12	1189	75.9	239	2	US-08-225- Sequence 6, Applicatio	3.04e-92
13	821	52.4	125	2	US-08-580- Sequence 20, Applicati	5.00e-60
14	821	52.4	125	1	US-08-225- Sequence 20, Applicati	5.00e-60
15	821	52.4	125	1	US-08-570- Sequence 20, Applicati	5.00e-60
16	639	40.8	130	2	US-08-580- Sequence 21, Applicati	3.02e-44
17	639	40.8	130	2	US-08-570- Sequence 21, Applicati	3.02e-44
18	639	40.8	130	1	US-08-225- Sequence 21, Applicati	3.02e-44
19	115	7.3	279	3	PCT-US95-0 Sequence 5, Applicatio	5.49e-01
20	112	7.2	156	4	5180811-2 Patent No. 5180811	8.95e-01
21	111	7.1	158	1	US-07-994- Sequence 98, Applicati	1.05e+00
22	111	7.1	281	2	US-08-810- Sequence 2, Applicatio	1.05e+00
23	111	7.1	281	3	PCT-US95-0 Sequence 2, Applicatio	1.05e+00

24	110	7.0	161	1	US-07-994- Sequence 61, Applicati	1.24e+00
25	110	7.0	162	1	US-07-994- Sequence 60, Applicati	1.24e+00
26	110	7.0	163	1	US-07-994- Sequence 64, Applicati	1.24e+00
27	108	6.9	155	1	US-07-994- Sequence 12, Applicati	1.71e+00
28	108	6.9	157	3	PCT-US95-0 Sequence 17, Applicati	1.71e+00
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30	108	6.9	157	2	US-08-394- Sequence 17, Applicati	1.71e+00
31	108	6.9	157	1	US-08-041- Sequence 2, Applicatio	1.71e+00
32	108	6.9	158	1	US-07-994- Sequence 86, Applicati	1.71e+00
33	108	6.9	158	1	US-07-994- Sequence 51, Applicati	1.71e+00
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35	108	6.9	158	1	US-08-397- Sequence 10, Applicati	1.71e+00
36	108	6.9	158	1	US-07-794- Sequence 5, Applicatio	1.71e+00
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44	108	6.9	233	4	5422425-2 Patent No. 5422425	1.71e+00
45	108	6.9	233	3	PCT-US95-1 Sequence 10, Applicati	1.71e+00

ALIGNMENTS

RESULT 1
ID US-08-570-923-23 STANDARD; PRT; 215 AA.
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AC
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DT
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DE
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Sequence 23, Application US/08570923
Sequence 23, Application US/08570923
Patent No. 5677430
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Armitage, Richard J.
APPLICANT: Gruss, Hans-Jurgen
TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kathryn A. Seese, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,923
FILING DATE: 12-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:

CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: NO. 5480981el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 215 AA; 24151 MW; 261175 CN;
Query Match 100.0%; Score 1566; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.76e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MHVPAGSVASHLGTSTRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDVPLKG 60
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Db 181 VNTTISVNVDTFOYIDTSTFFPLENVLISFIYLSNSD 215
QY 181 VNTTISVNVDTFOYIDTSTFFPLENVLISFIYLSNSD 215

RESULT 4

ID US-08-570-923-8 STANDARD; PRT; 234 AA.
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DT
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Sequence 8, Application US/08570923
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CC Sequence 8, Application US/08570923
CC Patent No. 5677430
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 234 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 234 AA; 26017 MW; 308679 CN;
Query Match 100.0%; Score 1566; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.76e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 20 MHVPAGSVASHLGTSTRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDVPLKG 79
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QY 1 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVVQRTDSIPNSPDNVPKLG 60
CC
DB 80 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSNWKDGLHGVRYQDGNLVIOFPGLY 139
CC
QY 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSNWKDGLHGVRYQDGNLVIOFPGLY 120
CC
DB 140 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMQTKHYQNLSQFLLDYIQ 199
CC
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMQTKHYQNLSQFLLDYIQ 180
CC
DB 200 VNTTISVNVDTFOYIDTSTFPLENLSIFLYSNSD 234
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QY 181 VNTTISVNVDTFOYIDTSTFPLENLSIFLYSNSD 215
CC
RESULT 5
ID US-08-580-014-8 STANDARD; PRT; 234 AA.
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AC xxxxxx
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DE Sequence 8, Application US/08580014
CC
CC Sequence 8, Application US/08580014
CC Patent No. 5753203
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580.014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
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CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225.989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US/07/966.775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
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CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 234 AA; 26017 MW; 308679 CN;
Query Match 100.0%; Score 1566; DB 2: Length 234;
Best Local Similarity 100.0%; Pred. No. 1.76e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 20 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVVQRTDSIPNSPDNVPKLG 79
QY 1 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVVQRTDSIPNSPDNVPKLG 60
DB 80 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSNWKDGLHGVRYQDGNLVIOFPGLY 139
QY 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSNWKDGLHGVRYQDGNLVIOFPGLY 120
DB 140 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMQTKHYQNLSQFLLDYIQ 199
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMQTKHYQNLSQFLLDYIQ 180
DB 200 VNTTISVNVDTFOYIDTSTFPLENLSIFLYSNSD 234
QY 181 VNTTISVNVDTFOYIDTSTFPLENLSIFLYSNSD 215
RESULT 6
ID US-08-225-989-8 STANDARD; PRT; 234 AA.
XX
AC xxxxxx
XX
XX
DT
XX
DE Sequence 8, Application US/08225989
XX
CC Sequence 8, Application US/08225989
CC Patent No. 5480981
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225.989
CC FILING DATE: 12 APRIL 1994
CC CLASSIFICATION: 435
CC
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:

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CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 234 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 234 AA; 26017 MW; 308679 CN;

Query Match 100.0%; Score 1566; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.76e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 MHVPAGSVASHLGTSTSYFLTTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 79
QY 1 MHVPAGSVASHLGTSTSYFLTTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 60

Db 80 GNCSEDLCLIKRAPFKSWAYLQVAKHLNKLKLSWKNKDGILHGVYQDGNLVQFPGLY 139
QY 61 GNCSEDLCLIKRAPFKSWAYLQVAKHLNKLKLSWKNKDGILHGVYQDGNLVQFPGLY 120

Db 140 FIICOLFVQCPNNSVDLKLLELHINKHKKQALVTVCSGQMKHYONLSQFLLDYLQ 199
QY 121 FIICOLFVQCPNNSVDLKLLELHINKHKKQALVTVCSGQMKHYONLSQFLLDYLQ 180

Db 200 VNTTISVNDVTFQYIDTSTFPLENLSIFLYSNSD 234
QY 181 VNTTISVNDVTFQYIDTSTFPLENLSIFLYSNSD 215

RESULT 7
ID US-08-570-923-19 STANDARD; PRT; 220 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 19, Application US/08570923
XX
CC Sequence 19, Application US/08570923
CC Patent No. 5677430
CC GENERAL INFORMATION:
CC APPLICANT: Goodwin, Raymond G.
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Armitage, Richard J.
CC APPLICANT: Gruss, Hans-Jurgen
CC TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
CC NUMBER OF SEQUENCES: 23
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
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CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,923
CC FILING DATE: 12-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 19:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 220 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 220 AA; 24724 MW; 283693 CN;

Query Match 75.9%; Score 1189; DB 1; Length 220;
Best Local Similarity 73.8%; Pred. No. 3.04e-92;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;

Db 20 STSRSYFYLTAL-VCLVAVAILVLVYQKKDSTPNTTERAPLKGKNCSEDLFCITLKS 78
QY 14 TTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPGKNCSEDLCLIKR 73

Db 79 TPSKKSWAYLQVSKHLNKLKLSWKNKDGILHGVYQDGNLVQFPGLYFIVCQLFVQCS 138
QY 74 APFKKSWAYLQVAKHLNKLKLSWKNKDGILHGVYQDGNLVQFPGLYFIVCQLFVQCP 133

Db 139 NHSVDLTQLLINSIKKOTLVTVCSGVQSKNIYONLSQFLHLYQVNSTISVRVDNFQ 198
QY 134 NNSVDLKLLELHINKHKKQALVTVCSGQMKHYONLSQFLLDYLQVNTTISVNDVTFQ 193

Db 199 YVDTNTFPLENLSIFLYSNSD 220
QY 194 YIDTSTFPLENLSIFLYSNSD 215

RESULT 8
ID US-08-225-989-19 STANDARD; PRT; 220 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 19, Application US/08225989
XX
CC Sequence 19, Application US/08225989
CC Patent No. 5480981
CC GENERAL INFORMATION:
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Query Match 75.9%; Score 1189; DB 2; Length 220;
Best Local Similarity 73.8%; Pred. No. 3.04e-92;
Matches 149; Conservative 34; Mismatches 18; Indels

Query Match 75.9%; Score 1189; DB 2; Length 220;
Best Local Similarity 73.8%; Pred. No. 3.04e-92;
Matches 149; Conservative 34; Mismatches 18; Indels

CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 239 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 239 AA; 26519 MW; 334382 CN;

Query Match 75.9%; Score 1189; DB 1; Length 239;
Best Local Similarity 73.8%; Pred. No. 3,04e-92;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;
Db 39 STSRSYFYLSTAL-VCLVAVAIILVYVQKKDSTPNTTEKAPLKGNCSEDLFCITLKS 97
QY 14 TTSRSYFYLTTATLALCLVFTVATIMLVVQRTDSTPNSPDNVPPLKGNCSEDLICILKR 73
Db 98 TPSKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIVQFPGLYFVLCQLFLVQCS 157
QY 74 APFKSWAYLQVAKHLNKTLSWNKDILHGVRQDGNLVQFPGLYFVLCQLFLVQCP 133
Db 158 NHSVDTLQLLINSKIKKQTLVTVCSGVQSKNIYQNLISQFLHYLQVNSTISVRVDNFQ 217
QY 134 NNSVDLKLLELLINKHKIKQALVTVCESGMQTKHVYQNLISQFLLDYLVQVNTTISVNDTFQ 193
Db 218 YVDTNTPFLDNVLSVFLYSND 239
QY 194 YIDTSTFPLENLSIFLYSND 215

RESULT 12
ID US-08-580-014-6 STANDARD; PRT; 239 AA.

XX xxxxxx

DE Sequence 6, Application US/08580014

XX Sequence 6, Application US/08580014
XX Patent No. 5753203

CC GENERAL INFORMATION:

CC APPLICANT: Goodwin, Raymond G.

CC APPLICANT: Smith, Craig A.

CC APPLICANT: Armitage, Richard J.

CC APPLICANT: Gruss, Hans-Jurgen

CC TITLE OF INVENTION: No. 5753203el cytokine That Binds CD30

CC NUMBER OF SEQUENCES: 23

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Kathryn A. Seese, Immunex Corporation

CC STREET: 51 University Street

CC CITY: Seattle

CC STATE: Washington

CC COUNTRY: USA

CC ZIP: 98101

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Apple 7.1
CC SOFTWARE: Microsoft Word, Version 5.1a
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/580,014
CC FILING DATE: 20-DEC-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/225,989
CC FILING DATE: 12 APRIL 1994
CC APPLICATION NUMBER: US 07/966,775
CC FILING DATE: 27-OCT-1992
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 907,224
CC FILING DATE: 01-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 899,660
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 892,459
CC FILING DATE: 02-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 889,717
CC FILING DATE: 26-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Seese, Kathryn A.
CC REGISTRATION NUMBER: 32,172
CC REFERENCE/DOCKET NUMBER: 2804-E
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206)587-0430
CC TELEFAX: (206)233-0644
CC TELEX: 756822
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 239 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 239 AA; 26519 MW; 334382 CN;

Query Match 75.9%; Score 1189; DB 2; Length 239;
Best Local Similarity 73.8%; Pred. No. 3,04e-92;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;

Db 39 STSRSYFYLSTAL-VCLVAVAIILVYVQKKDSTPNTTEKAPLKGNCSEDLFCITLKS 97
QY 14 TTSRSYFYLTTATLALCLVFTVATIMLVVQRTDSTPNSPDNVPPLKGNCSEDLICILKR 73
Db 98 TPSKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIVQFPGLYFVLCQLFLVQCS 157
QY 74 APFKSWAYLQVAKHLNKTLSWNKDILHGVRQDGNLVQFPGLYFVLCQLFLVQCP 133
Db 158 NHSVDTLQLLINSKIKKQTLVTVCSGVQSKNIYQNLISQFLHYLQVNSTISVRVDNFQ 217
QY 134 NNSVDLKLLELLINKHKIKQALVTVCESGMQTKHVYQNLISQFLLDYLVQVNTTISVNDTFQ 193
Db 218 YVDTNTPFLDNVLSVFLYSND 239
QY 194 YIDTSTFPLENLSIFLYSND 215

RESULT 13
ID US-08-580-014-20 STANDARD; PRT; 125 AA.

XX xxxxxx

XX Sequence 20, Application US/08580014

SQ SEQUENCE 125 AA; 13767 MW; 89412 CN;

Query Match 52.4%; Score 821; DB 1; Length 125;
Best Local Similarity 94.9%; Pred. No. 5.00e-60;
Matches 112; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db 7 HVPAGSEASHLGTTSRXYFYLTXTTALCLVFTVATIMVLVQRTSDIPNSPDNVLKGG 66
QY 2 HVPAGSVASHLGTTSRXYFYLTATLALCLVFTVATIMVLVQRTSDIPNSPDNVLKGG 61

Db 67 NCSEDLCLILKRAPFKKSWAYLQVXKHLNKTLSWKNKGILHGVRYODGNLVIQFPGF 124
QY 62 NCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYODGNLVIQFPGF 119

RESULT 15
ID US-08-570-923-20 STANDARD; PRT; 125 AA.
XX AC xxxxxx

Sequence 20, Application US/08570923

Sequence 20, Application US/08570923
Patent No. 5677430

GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Armitage, Richard J.
APPLICANT: Gruss, Hans-Jürgen
TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Seese, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570.923
FILING DATE: 12-DEC-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/225.989
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: US 07/966.775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907.224
FILING DATE: 01-JUL-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899.660
FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 892.459
FILING DATE: 02-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 889.717
FILING DATE: 26-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2804-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein fragment
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: huCD30 fragment (PRELIM)
SQ SEQUENCE 125 AA; 13767 MW; 89412 CN;

Query Match 52.4%; Score 821; DB 1; Length 125;
Best Local Similarity 94.9%; Pred. No. 5.00e-60;
Matches 112; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db 7 HVPAGSEASHLGTTSRXYFYLTXTTALCLVFTVATIMVLVQRTSDIPNSPDNVLKGG 66
QY 2 HVPAGSVASHLGTTSRXYFYLTATLALCLVFTVATIMVLVQRTSDIPNSPDNVLKGG 61

Db 67 NCSEDLCLILKRAPFKKSWAYLQVXKHLNKTLSWKNKGILHGVRYODGNLVIQFPGF 124
QY 62 NCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYODGNLVIQFPGF 119

Search completed: Fri Aug 13 16:54:30 1999
Job time : 10 secs.

WISORL

(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Aug 13 16:52:08 1999; Maspar time 11.07 Seconds
Tabular output not generated.

Title: >US-09-079-785-23
Description: (1-215) from US09079785.pep
Perfect Score: 1566
Sequence: 1 MHVPAGSVASHLGTTSRSYF.....DSTFPLENVLSIFLYNSD 215

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 44.814; Variance 91.007; scale 0.492

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	1566	100.0	234	2 A40710	CD30 ligand - human	1.68e-289	
2	1189	75.9	239	2 B40710	CD30 ligand - mouse	2.16e-211	
3	123	7.9	498	2 S52570	phosphoprotein phosph	5.18e-04	
4	117	7.5	499	2 A55346	phosphoprotein phosph	3.56e-03	
5	115	7.3	279	2 A53062	Fas ligand - mouse	6.68e-03	
6	113	7.2	234	2 J01344	tumor necrosis factor	1.25e-02	
7	111	7.1	281	2 I38707	Fas ligand - human	2.32e-02	
8	108	6.9	233	1 QWHUN	tumor necrosis factor	5.79e-02	
9	108	6.9	233	2 S22052	tumor necrosis factor	5.79e-02	
10	108	6.9	560	2 D69649	probable long-chain-f	5.79e-02	
11	106	6.8	278	2 A9266	Fas ligand - rat	1.06e-01	
12	104	6.6	232	2 S12606	tumor necrosis factor	1.92e-01	
13	100	6.4	379	2 A54433	tubulin--tyrosine lig	6.18e-01	
14	99	6.3	185	2 S52715	tumor necrosis factor	1.10e-00	
15	98	6.3	233	2 S11688	tumor necrosis factor	8.24e-01	
16	98	6.3	233	2 S24642	tumor necrosis factor	1.10e-00	
17	99	6.3	568	2 J55629	Muellerian-inhibiting	8.24e-01	
18	98	6.3	619	2 S34636	probable membrane pro	1.10e-00	
19	98	6.3	724	2 B71404	hypothetical protein	1.10e-00	
20	99	6.3	1684	2 T02632	hypothetical protein	8.24e-01	
21	97	6.2	235	2 J00029	tumor necrosis factor	1.45e-00	
22	95	6.1	228	2 S76711	hypothetical protein	2.55e-00	
23	95	6.1	249	2 S78166	H+-transporting ATP s	2.55e-00	

24	95	6.1	879	2 A56277	DNA-directed DNA poly	2.55e+00
25	94	6.0	281	2 F70700	hypothetical protein	3.36e+00
26	94	6.0	452	2 S72266	translational initiatio	3.36e+00
27	94	6.0	541	2 S42833	F40P12.4 protein - Ca	3.36e+00
28	94	6.0	650	2 S64939	CDC45 protein - yeast	3.36e+00
29	93	5.9	212	2 S62960	probable membrane pro	4.43e+00
30	92	5.9	235	1 QWNSN	tumor necrosis factor	5.82e+00
31	92	5.9	249	2 A64510	hypothetical protein	5.82e+00
32	92	5.9	407	2 JQ1654	SFR1 protein - human	5.82e+00
33	92	5.9	720	2 G64230	stringent response-li	5.82e+00
34	93	5.9	2496	2 A71616	secreted protein Pf52	4.43e+00
35	91	5.8	264	2 S77408	phosphoribosylaminoi	7.63e+00
36	89	5.7	483	2 T01053	hypothetical protein	1.30e+01
37	90	5.7	749	2 S13518	transposase Tam3 - ga	9.97e+00
38	89	5.7	769	2 S36657	SWI6 protein - yeast	1.30e+01
39	89	5.7	808	1 QPREX	glucose dehydrogenase	1.30e+01
40	88	5.6	276	2 B71907	hypothetical protein	1.69e+01
41	88	5.6	287	2 D70225	protein p23 homolog -	1.69e+01
42	88	5.6	309	2 I53384	4-1BB ligand - mouse	1.69e+01
43	88	5.6	382	2 B64158	hypothetical protein	1.69e+01
44	88	5.6	471	2 A41680	integral membrane pro	1.69e+01
45	88	5.6	1189	1 JC2366	protein-tyrosine-phos	1.69e+01

ALIGNMENTS

RESULT 1

ENTRY A40710 #type complete
TITLE CD30 ligand - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-1999

ACCESSIONS A40710
REFERENCE A40710
#authors Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrar, T.; Baker, E.; Sutherland, G.R.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Grabstein, K.H.; Gliniak, B.; McAllister, I.B.; Fanslow, W.; Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, R.J.

#journal Cell (1993) 73:1349-1360
#title CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand defines an emerging family of cytokines with homology to TNF.

#cross-references MUID:93313964
#accession A40710

##status preliminary
##molecule_type mRNA
##residues 1-234 #label SMI
##cross-references GB:L09753; NID:g349277; PID:g349278
#KEYWORDS cytokine receptor; membrane protein; surface antigen
#SUMMARY #length 234 #molecular-weight 26017 #checksum 1088

Query Match 100.0%; Score 1566; DB 2: Length 234;
Best Local Similarity 100.0%; Pred. No. 1.68e-289;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	20	MHVPAGSVASHLGTTSRSYFITTATLALCLVFTVATIMLVVQRTDSIPNSPDNPLKG	79
Qy	1	MHVPAGSVASHLGTTSRSYFITTATLALCLVFTVATIMLVVQRTDSIPNSPDNPLKG	60
Db	80	GNCSDDLCLIKRAPFKSWAYLQVAKHLNKTLSWKNKDGILHGVYQGNLVIQPFGLY	139
Qy	61	GNCSDDLCLIKRAPFKSWAYLQVAKHLNKTLSWKNKDGILHGVYQGNLVIQPFGLY	120
Db	140	FTICQLQFLVQCPNNSVDLKLLELLNKHKKOALYTVCESSGMQTRKHVYQNLQSOFLDYLQ	199
Qy	121	FTICQLQFLVQCPNNSVDLKLLELLNKHKKOALYTVCESSGMQTRKHVYQNLQSOFLDYLQ	180
Db	200	VNTTISVNDVFQYIDTSTFFPLENVLSIFLYNSD	234
Qy	181	VNTTISVNDVFQYIDTSTFFPLENVLSIFLYNSD	215

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RESULT 2
ENTRY B40710 #type complete
TITLE CD30 ligand - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-1999
ACCESSIONS B40710
REFERENCE Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrar, T.; Baker, E.; Sutherland, G.R.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Grabstein, K.H.; Gliniak, B.; McAllister, I.B.; Fanslow, W.; Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, R.J.
#journal (1993) 73:1349-1360
#title CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand defines an emerging family of cytokines with homology to TNF.
#cross-references MUID:93313964
#accession B40710
#status preliminary
#molecule_type mRNA
#residues 1-239 #label SMI
#cross-references GB:L09754; NID:g349288; PID:g349289
KEYWORDS cytokine receptor; membrane protein; surface antigen
SUMMARY #length 239 #molecular-weight 26519 #checksum 3403

Query Match 75.9% Score 1189; DB 2; Length 239;
Best Local Similarity 73.8%; Pred. No. 2.16e-211;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;

Db 39 STSRSFYLTAL-VCLVVAIVLIVVQKDSPTNTEKAPLKGNCSEDLFLTKS 97
QY 14 TTSRSFYLTALCLVFTVATIMLVVQRTDTPNSPDNVLKGGNCSEDLCLILR 73
Db 98 TPKSKSWAYLVQSKHNNTKLNSNEDTGLIYQDGLIVQPGLYFTVQQLQFLVQCS 157
QY 74 APEFKSWAYLVQAKHLNKLSKNKGILGVRYQDGLVQPGLYFTVQQLQFLVQCP 133
Db 158 NHSVDTLQLLINSKIKQTIVTCVSGVQSKNIYQNLQSLFLLHYLVQVNSTISVRVDNFQ 217
QY 134 NNSVDLKLLELLINKHKIKQALVTCVSGMQTKHVIYQNLQSLFLLDYLVQVNTISVVDTFQ 193
Db 218 YVDNTFFLDNVLVFLYSSSD 239
QY 194 YIDTSTFPLENVLFIYNSND 215

RESULT 3
ENTRY S52570 #type complete
TITLE phosphoprotein phosphatase (EC 3.1.3.16) 5, catalytic subunit - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 01-Aug-1995 #sequence_revision 02-Jul-1996 #text_change 17-Mar-1999
ACCESSIONS S52570
REFERENCE Chen, M.X.; McPartlin, A.E.; Brown, L.; Chen, Y.H.; Barker, H.M.; Cohen, P.T.W.
#journal EMBO J. (1994) 13:4278-4290
#title A novel human protein serine/threonine phosphatase, which possesses four tetratricopeptide repeat motifs and localizes to the nucleus.
#cross-references MUID:95009929
#accession S52570
#molecule_type mRNA
#residues 7-498 #label CH2
#cross-references EMBL:S73586; EMBL:X89416
#experimental_source teratocarcinoma cell line NTERA-2
REFERENCE PC4136
#authors Xu, X.L.; Lagercrantz, J.; Zickert, P.; Bajjalica-Lagercrantz,

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S.; Zetterberg, A.
Biochem. Biophys. Res. Commun. (1996) 218:514-517
Chromosomal localization and 5' sequence of the human protein serine/threonine phosphatase 5' gene.
#journal PC4136
#accession PC4136
#molecule_type mRNA
#residues 1-37 #label XUX
#cross-references EMBL:X92121; NID:g1177477; PID:e205526; PID:g1177478
#experimental_source fetal brain
GENETICS
#gene GDB:PPP5C; PPP5; PP5
#cross-references GDB:I36857
#map_position 19q13.3-19q13.3
FUNCTION
#description catalyzes the hydrolytic dephosphorylation of protein-phosphoserine and protein-phosphothreonine plays a role in the regulation of RNA synthesis and mitosis
#note #superfamily phosphoprotein phosphatase homology; phosphoesterase core homology; tetratricopeptide repeat homology
KEYWORDS iron; nucleus; phosphoric monoester hydrolase; zinc
FEATURE
28-61 #domain tetratricopeptide repeat homology #label TT1\
62-95 #domain tetratricopeptide repeat homology #label TT2\
96-129 #domain tetratricopeptide repeat homology #label TT3\
204-467 #domain phosphoprotein phosphatase homology #label PPP\
236-305 #domain phosphoesterase core homology #label PEC\
242,244,271 #binding_site iron (Asp, His, Asp) #status predicted\
271,303,352,426 #binding_site zinc (Asp, Asn, His, His) #status predicted\
274,304,450 #active_site Asp, His, Tyr #status predicted\
275,399 #binding_site substrate phosphate (Arg) #status predicted\
SUMMARY #length 498 #molecular-weight 56820 #checksum 5353

Query Match 7.9% Score 123; DB 2; Length 498;
Best Local Similarity 26.1%; Pred. No. 5.18e-04;
Matches 23; Conservative 28; Mismatches 31; Indels 6; Gaps 6;

Db 208 CAVQILVQV-KEVLS-KLSLTIVETTLKETKINVC-GDTHG-QFYDLLNIFELNGLPSET 263
QY 124 CQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTCVSGMQTKHVIYQNLQSLFLLDYLVQNT 183
Db 264 NPVI-FNG-DFVDRGSFSVEVILTFCF 289
QY 184 TISVNVDTFYIDTSTFPLENVLISFLY 211

RESULT 4
ENTRY A55346 #type complete
TITLE phosphoprotein phosphatase (EC 3.1.3.16) PPT - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-1999
ACCESSIONS A55346
REFERENCE Becker, W.; Kentrup, H.; Klumpp, S.; Schultz, J.E.; Joost, H.G.
#journal J. Biol. Chem. (1994) 269:22586-22592
#title Molecular cloning of a protein serine/threonine phosphatase containing a putative regulatory tetratricopeptide repeat domain.
#cross-references MUID:94357899
#accession A55346
#status preliminary
#molecule_type mRNA
#residues 1-499 #label BEC
#cross-references GB:X77237
#note authors translated the codon AAG for residue 53 as Gln, and GTA for residue 496 as Leu
CLASSIFICATION #superfamily phosphoprotein phosphatase homology; phosphoesterase core homology; tetratricopeptide repeat homology

```

```
#cross-references GB:M64087; NID:g164244; PID:g164245
COMMENT This protein is an important proximal mediator of endotoxemia.
GENETICS
#gene TNF-alpha
#introns 62/3; 79/1; 95/1
CLASSIFICATION #superfamily tumor necrosis factor
KEYWORDS cytokine; cytotoxic; glycoprotein; lymphokine; macrophage; membrane protein
FEATURE
78-234      #product tumor necrosis factor alpha #status predicted
            #label TUM
SUMMARY     #length 234 #molecular-weight 25469 #checksum 7690
Query Match       7.2%; Score 113; DB 2; Length 234;
Best Local Similarity 34.7%; Pred.No. 1.25e+02;
Matches          25; Conservative 16; Mismatches 25; Indels 6; Gaps 6;
Db    83 RTPSDKPVAV-VANPOAESQQLWLSGRNALLANGVKUTDNLVPLVDGLYLIYSVLFL 141
   | : | | : | | : | : | : | | : | | : | | : | | : | | : | | : |
Qy   73 RAFPKEWAYLQAHLNKTKLSW-N-K-DGIL-HGVRYQGDNLVITQFPGLYFIICOLF 128
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db   142 KGOGCPSTHYLL 153
   ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy  129 LVQ-CPNNNSVDL 139

RESULT      7
ENTRY      I38707      type complete
TITLE      Fas ligand - human
ORGANISM   Homo sapiens #common_name man
DATE       29-May-1998 #sequence_revision 29-May-1998 #text_change
           03-Aug-1998
ACCSIONS   I38707; JC2340; S57565; I38554
REFERENCE   Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
             Int. Immunol. (1994) 6:1567-1574
             Human Fas ligand: gene structure, chromosomal location and species specificity.
#cross-references MUID:95127550
#accession I38707
#status preliminary; translated from GB/EMBL/DDBJ
#molecule_type mRNA
#residues 1-281 ##label RES
#cross-references EMBL:U11821; NID:g595430; PID:g595431
REFERENCE   JC2340
#authors   Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kashihara, A.; Fusamoto, H.; Kamada, T.
Biochem. Biophys. Res. Commun. (1994) 204:468-474
#journal   Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
#title     Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
#cross-references MUID:95071350
#accession JC2340
#molecule_type DNA
#residues 1-281 ##label MIT
#cross-references GB:D38122; DDBT:D29820; NID:g601892; PID:d1007898; PID:g1369902
REFERENCE   S57565
#authors   Schatzlein, C.E.
#submission submitted to the EMBL Data Library, June 1995
#accession S57565
#status preliminary
#molecule_type mRNA
#residues 1-281 ##label SCH
#cross-references EMBL:X89102; NID:g887455; PID:g887456
REFERENCE   I38554
#authors   Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Goodwin, R.G.; Smith, C.A.; Ramsdell, F.; Lynch, D.H.
J. Exp. Med. (1995) 181:71-77
#journal   Fas ligand mediates activation-induced cell death in human T lymphocytes.
#title     Fas ligand mediates activation-induced cell death in human T lymphocytes.
#cross-references MUID:95105731
```

Strickler, J.: Van Arsdel, J.N.: Yamamoto, R.: Mark, D.F.
Science (1985) 228:149-154
Molecular cloning of the complementary DNA for human tumor
necrosis factor.
#cross-references MUID:85142190
#accession A4189
#molecule_type mRNA
#residues 1-62, 'S', 64-233 #label WAN
#cross-references GB:M10988; NID:g339737; PID:g339738
REFERENCE A61478
#authors Fukuda, S.; Ando, S.; Sanou, O.; Tanlai, M.; Fujii, M.;
Kusaki, N.; Nakamura, K.I.; Ando, O.; Torigoe, K.;
Sugimoto, T.; Kurimoto, M.
#journal Lymphokine Res. (1988) 7:175-185
#title Simultaneous production of natural human tumor necrosis
factor-alpha, -beta and interferon-alpha from BALL-1 cells
stimulated by HVJ.
#accession B61478
#molecule_type protein
#residues 83-102; 109-119; 121-128, 'X', 130-131; 142-144, 'X', 146,
'XXX', 150-152; 159-174; 180, 'X', 182-204 #label FUK
REFERENCE A92511
#authors Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer,
S.A.; Henzel, W.J.; Bringham, T.S.; Nedwin, G.E.; Goeddel,
D.V.; Harkins, R.N.
#journal J. Biol. Chem. (1985) 260:2345-2354
#title Human tumor necrosis factor. Production, purification, and
characterization.
#cross-references MUID:85130974
#contents annotation: disulfide bond
#accession I53311
#status translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-233 #label RES
#cross-references GB:M26331; NID:g339763; PID:g339764
#experimental_source U-937 cells
REFERENCE S62610
#authors Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
#journal Eur. J. Biochem. (1996) 235:431-437
#title O-Glycosylated species of natural human tumor-necrosis
factor-alpha.
#cross-references MUID:96202967
#accession S62610
#status preliminary
#molecule_type protein
#residues 77-99 #label TAK
COMMENT Secreted from mitogen-activated macrophages within 4-24 hours after
induction, TNF-alpha can cause cytotoxicity of certain tumor cell
lines and have an antiproliferative effect on others without
detriment to normal cells. It can also act synergistically with
interferon gamma to kill certain transformed cell lines.
COMMENT TNF-alpha and -beta (lymphotoxin) are the products of different
genes closely linked on chromosome 6. They are induced by similar
mitogenic stimuli and have similar biological activities but are
produced by different cell types and have different induction
kinetics.
GENETICS
#gene GDB:TNF; TNFA
#cross-references GDB:120441; OMIM:191160
#map_position 6p21.3-6p21.3
#introns 62/3; 78/1; 94/1
CLASSIFICATION #superfamily tumor necrosis factor
KEYWORDS cytokine; cytotoxin; glycoprotein; lymphokine; macrophage;
membrane protein
#product tumor necrosis factor #status experimental
77-233

```

145-177      #label MAT
SUMMARY      #disulfide_bonds #status experimental
              #length 233 #molecular_weight 25644 #checksum 6900

Query Match      6.9%; Score 108; DB 1; Length 233;
Best Local Similarity 36.1%; Pred. No. 5.79e-02;
Matches 26; Conservative 14; Mismatches 26; Indels 6; Gaps 5;

Db 82 RTPSKPVAHV-VANPQAEQOLWLNRRNALLANGVELRDNLVWPSEGLYLIYSQVLF 140
QY 73 RAPFKKSWAYLQVAKHLNKLKLSW-NK--DGIL-HGVRYQDGNLVLPFGYFIICQLQF 128

Db 141 KGQCCPSTHVLL 152
QY 129 LVQ-CPNNSVDL 139

RESULT 9
ENTRY   tumor necrosis factor - baboon
TITLE   #type complete
ORGANISM #formal_name Papio sp. #common_name baboon
DATE     20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
        08-Sep-1997
ACCESSIONS S22052
REFERENCE   S22052
#authors   Sanjanwala, M.; Edwards, A.
#submission submitted to the EMBL Data Library, September 1991
#description Baboon Tumor Necrosis Factor Derived from Sequences of
              Genomic DNA.
#accession S22052
##status   preliminary
##molecule_type DNA
##residues 1-233 #label SAN
##cross-references EMBL:A62141; NID:g38159; PID:g38160
GENETICS
#introns   62/3; 78/1; 94/1
CLASSIFICATION #superfamily tumor necrosis factor
KEYWORDS      transmembrane protein
SUMMARY       #length 233 #molecular_weight 25557 #checksum 6746

Query Match      6.9%; Score 108; DB 2; Length 233;
Best Local Similarity 36.1%; Pred. No. 5.79e-02;
Matches 26; Conservative 14; Mismatches 26; Indels 6; Gaps 5;

Db 82 RTPSKPVAHV-VANPQAEQOLWLNRRNALLANGVELRDNLVWPSEGLYLIYSQVLF 140
QY 73 RAPFKKSWAYLQVAKHLNKLKLSW-NK--DGIL-HGVRYQDGNLVLPFGYFIICQLQF 128

Db 141 KGQCCPSTHVLL 152
QY 129 LVQ-CPNNSVDL 139

RESULT 10
ENTRY   Probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) lcfa
TITLE   - Bacillus subtilis
ORGANISM #formal_name Bacillus subtilis
DATE     05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
        05-Feb-1999
ACCESSIONS D69649
REFERENCE   A69580
#authors   Kunst, F.; Ogasawara, N.; Mosser, I.; Albertini, A.M.;
              Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
              Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
              A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
              Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
              Chou, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
              Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
              Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.;
              Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
              M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
              S.; Glaser, P.; Goffeau, A.; Golligty, E.J.; Grandi, G.;

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Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaer-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maeel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott, G.;
A.M.; Prescan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;
Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo,
B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;
Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.;
Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.;
Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenecker, T.;
Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto,
K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;
Yoshikawa, H.; Danchin, A.
#journal     Nature (1997) 390:249-256
#title       The complete genome sequence of the Gram-positive bacterium
              Bacillus subtilis.
#cross-references MIMD:98044033
#accession   D69649
##status     preliminary; nucleic acid sequence not shown;
              translation not shown
##molecule_type DNA
##residues   1-560 #label KUN
##cross-references GB:299118; GB:AL009126; NID:g2635200; PID:ell84105;
              PID:g2635321
##experimental_source strain 168
GENETICS
#gene        lcfa
CLASSIFICATION #superfamily acetate--CoA ligase homology
KEYWORDS      acid-thiol ligase
FEATURES
70-549        #domain acetate--CoA ligase homology #label ACL
SUMMARY       #length 560 #molecular_weight 62691 #checksum 4760

Query Match      6.9%; Score 108; DB 2; Length 560;
Best Local Similarity 26.3%; Pred. No. 5.79e-02;
Matches 25; Conservative 24; Mismatches 42; Indels 4; Gaps 4;

Db 93 GVLF-AGGIVVQTNPLY-TEHELEVQLRDAQVSVITLIDLPKAKMKTLISIVQILIT 150
QY 104 GVRVODGNLVLPFGYFIICQLQFVQCPNNSVDKLELLINKHKKQALVTVCESGMQ 163

Db 151 SVKDYLPFPKNIL-YPLTKQKQKHIDFDKTAHIT 184
QY 164 TKHYQNLSQLLDY-LQVNTTISVNDTFQYIDT 197

RESULT 11
ENTRY   fas ligand - rat
TITLE   #type complete
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE     13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
        10-Sep-1997
ACCESSIONS A49266
REFERENCE   A49266
#authors   Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
#journal    Cell (1993) 75:1169-1178
#title      Molecular cloning and expression of the Fas ligand, a novel
              member of the tumor necrosis factor family.
#cross-references MIMD:94084792
#accession   A49266
##status     preliminary
##molecule_type mRNA

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QY 103 HGVRYQDGLVIOFPGLYFIICQLQLVQ-CPNNSV 137

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RESULT 15
ENTRY S11688 #type complete
TITLE tumor necrosis factor alpha - cat
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
      08-Sep-1997
ACCESSIONS S11688
REFERENCE S11688
#authors McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.;
      Rawlings, C.A.
#journal Nucleic Acids Res. (1990) 18:5563
#title Gene sequence of feline tumor necrosis factor alpha.
#cross-references MUID:91016860
#accession S11688
##status preliminary
##molecule_type DNA
##residues 1-233 #label MCG
##cross-references EMBL:X54000; NID:g1084; PID:g295777
GENETICS
#introns 62/3; 78/1; 94/1
CLASSIFICATION #superfamily tumor necrosis factor
KEYWORDS transmembrane protein
SUMMARY #length 233 #molecular-weight 25322 #checksum 5607

Query Match 6.3%; Score 99; DB 2; Length 233;
Best Local Similarity 36.7%; Pred. No. 8.24e-01;
Matches 18; Conservative 10; Mismatches 19; Indels 2; Gaps 2;

Db 104 RLSRANALLANGVELTDNOLKVPDGLYLIYSQVLEFGQCPSTHVL 152
:||||:|||||:|:|:|||||:|:|:|:|:|
QY 93 KLSWNKDGL-HGVRYQDGLVIOFPGLYFIICQLQLVQ-CPNNSVDL 139

```

Search completed: Fri Aug 13 16:52:28 1999
Job time : 20 secs.

W P I R E

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:52:45 1999; MasPar time 7.74 seconds
Tabular output not generated.

Title: >US-09-079-785-23
Description: (1-215) from US09079785.pep
Perfect Score: 1566
Sequence: 1 MHVPAGSVASHLIGTTSRYF.....DTSTFPLENVLIFLYNSD 215

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss:prot37
1:swissprot

Statistics: Mean 45.932; Variance 79.659; scale 0.577

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1566	100.0	234	1	CD3L_HUMAN CD30 LIGAND (CD30-L) (0.00e+00
2	1189	75.9	239	1	CD3L_MOUSE CD30 LIGAND (CD30-L).	3.65e-247
3	123	7.9	499	1	PPP5_HUMAN SERINE/THREONINE PROTE	3.73e-05
4	117	7.5	499	1	PPP5_RAT SERINE/THREONINE PROTE	3.41e-04
5	115	7.3	279	1	FASL_MOUSE FAS ANTIGEN LIGAND	7.02e-04
6	113	7.2	234	1	TNFA_MOUSE TUMOR NECROSIS FACTOR	1.44e-03
7	111	7.1	281	1	FASL_HUMAN FAS ANTIGEN LIGAND (AP	2.92e-03
8	110	7.0	233	1	TNFA_MACMU TUMOR NECROSIS FACTOR	4.15e-03
9	108	6.9	233	1	TNFA_HUMAN TUMOR NECROSIS FACTOR	8.33e-03
10	108	6.9	233	1	TNFA_PAPSP TUMOR NECROSIS FACTOR	8.33e-03
11	108	6.9	560	1	LCFA_BACSU LONG-CHAIN-FATTY-ACID-	8.33e-03
12	106	6.8	233	1	TNFA_PAPHU TUMOR NECROSIS FACTOR	1.66e-02
13	106	6.8	278	1	FASL_RAT FAS ANTIGEN LIGAND	1.66e-02
14	104	6.6	232	1	TNFA_PIG TUMOR NECROSIS FACTOR	3.28e-02
15	103	6.6	233	1	TNFA_MACFA TUMOR NECROSIS FACTOR	4.59e-02
16	102	6.5	233	1	TNFA_CANFA TUMOR NECROSIS FACTOR	6.42e-02
17	100	6.4	379	1	TTL_PIG TUBULIN--TYROSINE LIGA	1.24e-01
18	101	6.4	2670	1	YAQS_SCHPO PUTATIVE TRANSLATIONAL	8.95e-02
19	98	6.3	229	1	TNFA_CEREL TUMOR NECROSIS FACTOR	2.39e-01
20	99	6.3	233	1	TNFA_FELCA TUMOR NECROSIS FACTOR	1.73e-01
21	98	6.3	233	1	TNFA_BOVIN TUMOR NECROSIS FACTOR	2.39e-01
22	97	6.2	235	1	TNFA_RAT TUMOR NECROSIS FACTOR	3.30e-01
23	97	6.2	377	1	TTL_BOVIN TUBULIN--TYROSINE LIGA	3.30e-01

24	94	6.0	452	1	E2BG_RAT	TRANSLATION INITIATION	8.57e-01
25	94	6.0	650	1	CC45_YEAST	CELL DIVISION CONTROL	8.57e-01
26	93	5.9	79	1	YF71_HAEIN	HYPOTHETICAL PROTEIN H	1.17e+00
27	93	5.9	212	1	YND8_YEAST	HYPOTHETICAL 24.7 KD P	1.17e+00
28	92	5.9	235	1	TNFA_MOUSE	TUMOR NECROSIS FACTOR	1.60e+00
29	92	5.9	249	1	Y201_METJA	HYPOTHETICAL PROTEIN M	1.60e+00
30	93	5.9	291	1	TRAI_MOUSE	TNF-RELATED APOPTOSIS	1.17e+00
31	92	5.9	375	1	GM12_SCHPO	ALPHA-1,2-GALACTOSYLTR	1.60e+00
32	92	5.9	436	1	VU10_HSV6U	U10 PROTEIN.	1.60e+00
33	92	5.9	720	1	SPOT_MYCGE	PROBABLE GUANOSINE-3',	1.60e+00
34	89	5.7	234	1	TNFA_CAVPO	TUMOR NECROSIS FACTOR	3.98e+00
35	89	5.7	769	1	SWI6_KLULA	REGULATORY PROTEIN SWI	3.98e+00
36	89	5.7	808	1	DHG_GLUOX	GLUCOSE DEHYDROGENASE	3.98e+00
37	88	5.6	301	1	SGO2_YEAST	SCO2 PROTEIN PRECURSOR	5.36e+00
38	88	5.6	309	1	41BL_MOUSE	4-1BL LIGAND (4-1BL).	5.36e+00
39	88	5.6	382	1	Y753_HAEIN	HYPOTHETICAL PROTEIN H	5.36e+00
40	88	5.6	471	1	PSS1_CRILQ	PHOSPHATIDYL SERINE SYN	5.36e+00
41	88	5.6	473	1	PSS1_HUMAN	PHOSPHATIDYL SERINE SYN	5.36e+00
42	88	5.6	531	1	TCPY_MOUSE	T-COMPLEX PROTEIN 1, Z	5.36e+00
43	88	5.6	678	1	GARP_PLAUF	GLUTAMIC ACID-RICH PRO	5.36e+00
44	88	5.6	1189	1	PTNE_MOUSE	PROTEIN-TYROSINE PHOSP	5.36e+00
45	88	5.6	1202	1	YE01_SCHPO	HYPOTHETICAL 138.5 KD	5.36e+00

ALIGNMENTS

RESULT	ID	CD3L_HUMAN	STANDARD	PRT	234 AA.
AC	P32971;				
DT	01-OCT-1993 (REL. 27, CREATED)				
DT	01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)				
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)				
DE	CD30 LIGAND (CD30-L) (CD153 ANTIGEN).				
GN	CD30LG OR CD30L.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;				
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 93313964.				
RA	SMITH C.A., GRUSS H.-J., DAVIS T., ANDERSON D., FARRAH T.,				
RA	BAKER E., SUTHERLAND G.R., BRANNAN C.I., COPELAND N.G., JENKINS N.A.,				
RA	GRABSTEIN K.H., GLINKA B., MCALISTER I.B., FANLOW W., ALDERSON M.,				
RA	FALK B., GIMPEL S., GILLIS S., DIN W.S., GOODWIN R.G., ARMITAGE R.J.;				
RT	*CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose				
RT	ligand defines an emerging family of cytokines with homology to				
RT	TNF.*;				
RL	CELL 73:1349-1360(1993).				
CC	-1- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF				
CC	T CELLS.				
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.				
CC	-1- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry;				
CC	WWW="http://www.ncbi.nlm.nih.gov/ptow/cd/cd153.htm".				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; L09753; G349278; -				
DR	PIR; A40710; A40710.				
DR	PROSITE; PS00251; TNF_1; 1.				
DR	PROSITE; PS50049; TNF_2; 1.				
DR	PFAM; PF00229; TNF; 1.				
DR	CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.				
KW	DOMAIN 1 37				
FT	TRANSNEM 38 62				
FT	DOMAIN 53 234				
FT	DOMAIN 63 81				
FT	CARBOHYD 81				
FT	POTENTIAL.				

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FT CARBOHYD 109 109 POTENTIAL.
FT CARBOHYD 153 153 POTENTIAL.
FT CARBOHYD 189 189 POTENTIAL.
FT CARBOHYD 201 201 POTENTIAL.
SQ SEQUENCE 234 AA; 26017 MW; A77E97B1 CRC32;
Query Match 100.0%; Score 1566; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 20 MHVPGASVASHLGTSTRSYFTTATLALCLVFTVATIMLVVQRTDIPNSPDNVLPLG 79
QY 1 MHVPGASVASHLGTSTRSYFTTATLALCLVFTVATIMLVVQRTDIPNSPDNVLPLG 60
Db 80 GNCSEDLICILRAPEKKSWAYLOVAKHLNKTLSWNGDILHGVYQDNLVIOFPGLY 139
QY 61 GNCSEDLICILRAPEKKSWAYLOVAKHLNKTLSWNGDILHGVYQDNLVIOFPGLY 120
Db 140 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCSGQMTKHYQNLQSLFLDYLYQ 199
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCSGQMTKHYQNLQSLFLDYLYQ 180
Db 200 VNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234
QY 181 VNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 215
RESULT 2
ID CD3L_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CD30 LIGAND (CD30-L).
GN CD30L OR CD30L.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-T-CELL;
RX MEDLINE; 9313964.
RA SMITH C.A., GRUEN H.-J., DAVIS T., ANDERSON D., FARRAH T.,
RA BAKER E., SUTHERLAND G.R., BRANNAN C.I., COPELAND N.G., JENKINS N.A.,
RA GRABSTEIN K.H., GLINKA B., MCALISTER I.B., FANSLAW W., ALDERSON M.,
RA FALK B., GIMPEL S., GILLIS S., DIN W.S., GOODWIN R.G., ARMITAGE R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF."
RL CELL 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L09754; G349289; -
DR PIR; B40710; B40710.
DR MGD; MGI:88328; CD30L.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR PFAM; PF00229; TNF; 1.
KW CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
FT DOMAIN 1 43
FT TRANSMEM 44 67
FT DOMAIN 68 239
EXTRACELLULAR (POTENTIAL).
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FT CARBOHYD 75 75 POTENTIAL.
FT CARBOHYD 86 86 POTENTIAL.
FT CARBOHYD 114 114 POTENTIAL.
FT CARBOHYD 158 158 POTENTIAL.
FT CARBOHYD 194 194 POTENTIAL.
FT CARBOHYD 206 206 POTENTIAL.
SQ SEQUENCE 239 AA; 1EB8A11D CRC32;
Query Match 75.98; Score 1189; DB 1; Length 239;
Best Local Similarity 73.8%; Pred. No. 3.55e-247;
Matches 149; Conservative 34; Mismatches 18; Indels 1; Gaps 1;
Db 39 TSRSFYSTTAL-VCLVVAVALIIVVQKDKSPNTEKAPLKGKNGSEDLFLTKLS 97
QY 14 TSRSFYSTTALVCLVFTVATIMLVVQRTDIPNSPDNVLPLKNGSEDLFLTKLR 73
Db 98 TPSKKSWAYLOVAKHLNKTLSWNGDILHGVYQDNLVIOFPGLYFVQCQLFVQCS 157
QY 74 APEKKSWAYLOVAKHLNKTLSWNGDILHGVYQDNLVIOFPGLYFVQCQLFVQCP 133
Db 158 NHSVDTLQILLINKSKKQTLVTVCSGQSKNIYQNLQSLFLHLYQVNSTISVVDNFQ 217
QY 134 NNSVDLKLLELLINKHKKQALVTVCSGQMTKHYQNLQSLFLDYLYQVNTTISVNVDTFO 193
Db 218 YVDTNTFFPLDNVLSVLYSSSD 239
QY 194 YVDTNTFFPLDNVLSVLYSSSD 215
RESULT 3
ID PPP5_HUMAN STANDARD; PRT; 499 AA.
AC P53041; Q16722;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN
DE PHOSPHATASE T) (PP-T) (PPT).
GN PPP5C OR PPP5.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE OF 7-499 FROM N.A.
RX MEDLINE; 95009929.
RA CHEN M.X., MCPARTLIN A.E., BROWN L., CHEN Y.H., BARKER H.M.,
RA COHEN P.T.W.;
RT "A novel human protein serine/threonine phosphatase, which possesses
RT four tetrapeptide repeat motifs and localizes to the nucleus."
RL EMO J. 13:4278-4290(1994).
RN [2]
RP SEQUENCE OF 9-499 FROM N.A.
RC TISSUE-FETAL BRAIN;
RX MEDLINE; 96115607.
RA YONG W.H., UEKI K., CHOU D., REEVES S.A., VON DEIMLING A.,
RA GUSILLA J.F., MOHREWEISER H.W., BUCKLER A.J., LOUIS D.N.;
RT "Cloning of a highly conserved human protein serine-threonine
RT phosphatase gene from the glioma candidate region on chromosome
RT 19q13.3."
RN [3]
RP GENOMICS 29:533-536(1995).
RC SEQUENCE OF 1-37 FROM N.A.
RX TISSUE-FETAL BRAIN;
RX MEDLINE; 96144708.
RA XU X., LAGERCRANTZ J., ZICKERT P., BAJALICA-LAGERCRANTZ S.,
RA ZETTERBERG A.;
RT "Chromosomal localization and 5' sequence of the human protein
RT serine/threonine phosphatase 5 gene."
RL BIOCHEM. BIOPHYS. RES. COMMUN. 218:514-517(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS) OF 19-177.
RX MEDLINE; 98151343.
RA DAS A.K., COHEN P.W., BARFORD D.;
RT "The structure of the tetrapeptide repeats of protein
```


CELL 76:969-976(1994).

[2]
SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELLING.
STRAIN-C57BL/6;
MEDLINE: 95388076.
RA PEITSCH M.J., TSCHOPP J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
of the TNF family.";
RL MOL. IMMUNOL. 32:761-772(1995).
[3]
SEQUENCE FROM N.A.
RX MEDLINE: 95196085.
RA LYNCH D.H., WATSON M.L., ALDERSON M.R., BAUM P.R., MILLER R.E.,
RA TOUCH T., GIBSON M., DAVIS-SMITH T., SMITH C.A., HUNTER K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
TNF family gene cluster.";
RL IMMUNITY 1:131-136(1994).
[4]
CHARACTERIZATION OF VARIANT GLD.
RX MEDLINE: 96091792.
RA HAHNE M., PEITSCH M.C., IRMLER M., SCHROETER M., LOWIN B.,
RA ROUSSEAU M., BRON C., RENNO T., FRENCH L., TSCHOPP J.;
RT "Characterization of the non-functional Fas ligand of gld mice.";
RL INT. IMMUNOL. 7:1381-1386(1995).
CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
T CELLS, OR BOTH.
CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FROM THE CELL
SURFACE.
CC -!- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR EMBL: U06948; G473565; -.
DR EMBL: U10984; G511222; -.
DR EMBL: S76752; G913760; -.
DR MGI: 9255; FASL.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR PFAM: PF00229; TNF; 1.
DR HSP: P01375; 2TUN.
KW CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR; APOPTOSIS;
DISEASE MUTATION.
KW DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 4 69 PRO-RICH.
FT DOMAIN 45 51 POLY-PRO.
FT DISULFID 200 231 BY SIMILARITY.
FT VARIANT 273 F -> L (IN GLD); ABOLISH BINDING OF FASL TO
ITS RECEPTOR).
FT CARBOHYD 117 117 POTENTIAL.
FT CARBOHYD 182 182 POTENTIAL.
FT CARBOHYD 248 248 POTENTIAL.
FT CARBOHYD 258 258 POTENTIAL.
SQ SEQUENCE 279 AA; 31442 MW; AFD84D4B CRC32;

Query Match 7.3%; Score 115; DB 1; Length 279;
Best Local Similarity 35.4%; Pred. No. 7.02e-04;

Matches 23; Conservative 8; Mismatches 30; Indels 4; Gaps 4;

Db 145 AHLTGNPHSRISPLEWEDTYGTALISGVKKYKGLVINETGLYFYVYKVGOSCCNQP 204
QY 81 AYLOVAKHLNKLKLSWNRD-GI-L-HGVRYODGNLVIOFPGLYFICQLQFLVQ-CPNNS 136
Db 205 LNHKV 209
QY 137 VDLKL 141

RESULT 6
ID TNFA_HORSE STANDARD; PRT; 234 AA.
AC P29553;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNFA.
OS EQUUS CABALLUS (HORSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PERISSODACTYLA; EQUIDAE; EQUUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92084125.
RA SU X., MORRIS D.D., MCGRAW R.A.;
RT "Cloning and characterization of gene TNF alpha encoding equine tumor
necrosis factor alpha.";
RL GENE 107:319-321(1991).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CACHECTIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
PROTEOLYTIC PROCESSING.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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DR EMBL: M64087; G164245; -.
DR PIR: JQ1344; JQ1344.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR PFAM: PF00229; TNF; 1.
DR HSP: P01375; ITNF.
DR CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
KW PROPEP 1 77 BY SIMILARITY.
FT CHAIN 78 234 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 146 178 BY SIMILARITY.
SQ SEQUENCE 234 AA; 25469 MW; CD20BE6E CRC32;

Query Match 7.2%; Score 113; DB 1; Length 234;
Best Local Similarity 34.7%; Pred. No. 1.44e-03;
Matches 25; Conservative 16; Mismatches 25; Indels 6; Gaps 6;

Db 83 RTPSDKPAHV-VANPOAEQOLWLSGRANALLANGVKLTNQLVPLDGLYISQVLF 141
QY 73 RAPFKKSWAYLQVAKHLNKLKLSW-N-K-DGIL-HGVRYODGNLVIOFPGLYFICQLQF 128
Db 142 KGQCPSTHVL 153

MEDLINE; 86030296.
MARMENOUT A., FRANSEN L., TAVERNIER J., DER HEYDEN J., TIGARD R.,
KAWASHIMA E., SHAW A., JOHNSON M.J., SEMON D., MUELLER R.,
RUYSSCHAERT M.R., VAN VLIET A., FIERIS W.;
"Molecular cloning and expression of human tumor necrosis factor and
comparison with mouse tumor necrosis factor.";
EUR. J. BIOCHEM. 152:515-522(1985).
[7]
SEQUENCE FROM N.A.
MEDLINE; 93272029.
IRIS F.J.M., BOUGUELERET L., PRIEUR S., CATERINA D., PRIMAS G.,
PERROT V., JURKA J., RODRIGUEZ-TOME P., CLAVIERIE J.-M., DAUSSET J.,
COHEN D.;
"dense Alu clustering and a potential new member of the NF kappa B
family within a 90 kilobase HLA class III segment.";
NAT. GENET. 3:137-145(1993).
[8]
X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE; 89159409.
JONES E.Y., STUART D.I., WALKER N.P.;
"Structure of tumour necrosis factor";
NATURE 338:225-228(1989).
[9]
X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE; 91193276.
JONES E.Y., STUART D.I., WALKER N.P.;
"The structure of tumour necrosis factor -- implications for
biological function.";
J. CELL SCI. SUPPL. 13:11-18(1990).
[10]
X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE; 90008932.
ECK M.J., SPRANG S.R.;
"The structure of tumour necrosis factor-alpha at 2.6-A resolution.
Implications for receptor binding";
J. BIOL. CHEM. 264:17595-17605(1989).
[11]
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT ARG-107.
MEDLINE; 98147459.
REED C., FU Z.Q., WU J., XUE Y.N., HARRISON R.W., CHEN M.J.,
WEBER I.T.;
"Crystal structure of TNF-alpha mutant R31D with greater affinity for
receptor R1 compared with R2.";
PROTEIN ENG. 10:1101-1107(1997).
[12]
X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT M3S.
MEDLINE; 98113178.
CHO H.S., SHIN N.K., JEONG W., SHIN H.C.,
KIM S.-S., KIM J.S., OH B.H.;
"High resolution crystal structure of a human tumor necrosis factor-
alpha mutant with low systemic toxicity.";
J. BIOL. CHEM. 273:2153-2160(1998).
[13]
MUTAGENESIS.
MEDLINE; 91184128.
OSTADE X.V., TAVERNIER J., PRANGE T., FIERIS W.;
"Localization of the active site of human tumour necrosis factor
(hTNF) by mutational analysis.";
EMBO J. 10:827-836(1991).
[14]
MYRISTOYLATION.
MEDLINE; 93018820.
STEVENSON F.T., BURSTEN S.L., LOCKSLEY R.M., LOVETT D.H.;
"Myristyl acylation of the tumor necrosis factor alpha precursor on
specific lysine residues";
J. EXP. MED. 176:1053-1062(1992).
[15]
FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CACHEXIA, IT IS A POTENT PROGEN CAUSING FEVER BY DIRECT ACTION
OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CONDITIONS.

Query Match 6.9%; Score 108; DB 1; Length 233;
Best Local Similarity 36.1%; Pred. No. 8.33e-03;
Matches 26; Conservative 14; Mismatches 26; Indels 6; Gaps 5;

Dd 82 RTPSDKPAHV-VANPOAQEQLOWLNRANALLANGVELRDQLNLPSEGLIYISQVLF 140
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 73 RAPEFKWAVLQVAHLNKTKLSW--DGIL-HGVRYDGNLVIOFPGLFYICOLQF 128
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 141 KGQCPSHTVLL 152
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 129 LVQ-CPANSVDL 139
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 10

ID	TNFA.PAPSP	STANDARD;	PRT;	233 AA.
AC	P33620;			
DT	01-FEB-1994 (REL. 28, CREATED)			
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).			
GN	TNFA.			
OS	PAPIO SP. (BABOON).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
OC	PRIMATES; CATARRHINI; CERCOPTHECIDAE; CERCOPTHECINAE; PAPIO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	SANJANWALA M., EDWARDS A.			
RL	SUBMITTED (SEP-1991) TO EMBL/GENBANK/DBJ DATA BANKS.			
CC	-1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN CONDITIONS.			
CC	-1- SUBUNIT: HOMOTRIMER.			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.			
CC	-1- PM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTOLYTIC PROCESSING.			
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL: X62141; G38160; .			
DR	PIR: S22052; S22052.			
DR	PROSITE; PS00251; TNF_1; 1.			
DR	PROSITE; PS00049; TNF_2; 1.			
DR	PFAM; PF00229; TNF; 1.			
DR	HSSP; P01375; TNF.			
KW	CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR; MYRISTYLATION.			
KW	FT PROPEP 1 76			
FT	CHAIN 77 233			
FT	TRANSMEM 36 56			
FT	LIPID 19 19			
FT	LIPID 20 20			
FT	LIPID 145 177			
FT	DISULFID 145 177			
FT	SEQUENCE 233 AA; 25557 MW; 7F049248 CRC32;			
SQ				

Query Match 6.9%; Score 108; DB 1; Length 233;
Best Local Similarity 36.1%; Pred. No. 8.33e-03;
Matches 26; Conservative 14; Mismatches 26; Indels 6; Gaps 5;

Dd 82 RTPSDKPAHV-VANPOAQEQLOWLNRANALLANGVELRDQLNLPSEGLIYISQVLF 140
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 73 RAPEFKWAVLQVAHLNKTKLSW--DGIL-HGVRYDGNLVIOFPGLFYICOLQF 128
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 141 KGQCPSHTVLL 152
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 129 LVQ-CPANSVDL 139
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY 73 RAPFKRSWAYLQVAKHLNKTLSW-NK--DGIL-HGVRYQDGNLVIOFPGLYFIICQLQF 128

Db 141 KGOGCPSTHVL 152

QY 129 LVQ-CPNNSVDL 139

RESULT 11

Id LCFA_BACSU STANDARD; PRT; 560 AA.

AC P94547;

DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE LONG-CHAIN-FATTY-ACID--COA LIGASE (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE).

DE SYNTHETASE).

GN LCFA.

OS BACILLUS SUBTILIS.

OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;

OC BACILLUS.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-168;

RX MEDLINE; 97124191.

RA WIPAT A., CARTER N., BRIGNELL C.S., GUY J.B., PIPER K.,

RA SANDERS J., EMMERSON P.T., HARWOOD C.R.;

RT "The dnaB-pheA (256 degrees-240 degrees) region of the Bacillus subtilis chromosome containing genes responsible for stress responses, the utilization of plant cell walls and primary metabolism."

RT MICROBIOLOGY 142:3067-3078(1996).

RL -!- CATALYTIC ACTIVITY: ATP + A LONG-CHAIN CARBOXYLIC ACID + AMP = AMP + PYROPHOSPHATE + AN ACYL-COA.

CC -!- COFACTOR: REQUIRES MAGNESIUM (BY SIMILARITY).

CC -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.

CC -----

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CC -----

CC EMBL; 275208; E1165333; -.

DR EMBL; 299118; E1184103; -.

DR SUBTILIST; BG11946; LCFA.

DR PROSITE; P500455; AMP BINDING; 1.

DR PFAM; PF00501; AMP-binding; 1.

DR HSP; P08659; 1LCI.

KW LIGASE; FATTY ACID METABOLISM; MAGNESIUM.

SQ SEQUENCE 560 AA; 62691 MW; 232B0115 CRC32;

Query Match 6.9%; Score 108; DB 1; Length 560;

Best Local Similarity 26.3%; Pred. No. 8.33e-03;

Matches 25; Conservative 24; Mismatches 42; Indels 4; Gaps 4;

Db 93 GVLF-AGGIVQNPPLY-TEHELEYQLRDAQSVIITLDLFPKAKMKTLSIVDQILIT 150

QY 104 GVRQDGNLVIOFPGLYFIICQLQFLVQCPNNSVDLKLLEINKHKIKQALVTVCESGMQ 163

Db 151 SVKDYLPFFKNIL-YPLTQKQKHIDFDKTANTHT 184

QY 164 TRHYQNLQSLQFLDY-LQVNTTISVNDVTFQYIDT 197

RESULT 12

Id TNFA_PAPHU STANDARD; PRT; 233 AA.

AC 077510;

DT 15-DEC-1998 (REL. 37, CREATED)

DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).

GN TNFA.

OS PAPIO HAMADRYAS URSINUS (CHACMA BABOON).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC PRIMATES; CATARRHINI; CERCOPITHECIDAE; CERCOPITHECINAE; PAPIO.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 98147379.

RA HAUDEK S.B., REDL H., SCHLAG G., GIROIR B.P.;

RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor alpha."

RL MOL. IMMUNOL. 34:1041-1042(1997).

CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN CONDITIONS.

CC -!- SUBUNIT: HOMOTRIMER.

CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.

CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.

CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.

CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

CC -----

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CC -----

CC EMBL; AF019963; G3417555; -.

DR PROSITE; P500251; TNF.1; 1.

DR PROSITE; P50049; TNF.2; 1.

KW CYTOKINE; CYTOTOXIN; 76 BY SIMILARITY.

FT PROPEP 1 76 TUMOR NECROSIS FACTOR.

FT CHAIN 77 233 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT DISULFID 145 177 BY SIMILARITY.

SQ SEQUENCE 233 AA; 25658 MW; E38CF6E8 CRC32;

Query Match 6.8%; Score 106; DB 1; Length 233;

Best Local Similarity 39.6%; Pred. No. 1.66e-02;

Matches 19; Conservative 10; Mismatches 17; Indels 2; Gaps 2;

Db 105 LNRRANALLANGVELTDNLVVPSEGLYLYSQVLPKGGQCPSHVLL 152

QY 94 LSNKDGIL-HGVRYQDGNLVIOFPGLYFIICQLQFLVQ-CPNNSVDL 139

RESULT 13

Id FASL_RAT STANDARD; PRT; 278 AA.

AC P36940;

DT 01-JUN-1994 (REL. 29, CREATED)

DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE FAS ANTIGEN LIGAND.

GN APTLGI OR FASL.

OC RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 94084792.

RA SUDA T., TAKAHASHI T., GOLSTEIN P., NAGATA S.;

RT "Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family."

RT of the tumor necrosis factor family."

RL CELL 75:1169-1178(1993).

CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC KIDNEY AND LUNG.
CC -!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
CC EMBL; U03470; G440179; -.
CC DR PROSITE; PS00251; TNF_1; 1.
CC DR PROSITE; PS50049; TNF_2; 1.
CC DR PFAM; PF00229; TNF; 1.
CC KW CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR; APOPTOSIS.
FT DOMAIN 1 77 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 78 99 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 100 278 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 4 69 PRO-RICH.
FT DOMAIN 45 58 POLY-PRO.
FT DISULFID 199 230 BY SIMILARITY.
FT CARBOHYD 116 116 POTENTIAL.
FT CARBOHYD 247 247 POTENTIAL.
FT CARBOHYD 257 257 POTENTIAL.
FT CARBOHYD 116 116 POTENTIAL.
FT CARBOHYD 247 247 POTENTIAL.
FT CARBOHYD 257 257 POTENTIAL.
SQ SEQUENCE 278 AA; 31140 MW; 6DC17725 CRC32;

Query Match 6.88; Score 106; DB 1; Length 278;
Best Local Similarity 36.38; Pred. No. 1.66e-02;
Matches 19; Conservative 9; Mismatches 20; Indels 4; Gaps 4;

Db 157 LEWEDYGTALISGVKYGKGLVINEAGLYFVYKVFYRGSCNSOPLSHKV 208
QY 94 LSNKND-GI-L-HGVRYQDGNLVIOFPGLYFIICQLQFLVQ-CPNNSVDLKL 141

RESULT 14
ID TNFA_PIG STANDARD; PRT; 232 AA.
AC P23563;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNFA.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLIA; SUIFORMES; SUINA; SUIDAE; SUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91016861.
RA DREWS R.T., COFFEE B.W., PRESTWOOD A.K., MCGRAW R.A.;
RT "Gene sequence of porcine tumor necrosis factor alpha."
RL NUCLEIC ACIDS RES. 18:5564-5564(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE; 91340150.

RA KUNERT P., WUEHRICH C., PETERHANS E., PAULI U.;
RT "The porcine tumor necrosis factor-encoding genes: sequence and
RT comparative analysis."
RL GENE 102:171-178(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=MACROPHAGE;
RA CHOI C.S., MOLLITOR T.W., LIN G.F., MURTAUGH M.P.;
RT "Complete nucleotide sequence of a cDNA encoding porcine tumor
RT necrosis factor-alpha."
RL ANIM. BIOTECHNOL. 2:97-105(1991).
RN [4]
RP SEQUENCE OF 44-232 FROM N.A.
RX MEDLINE; 90034181.
RA PAULI U., BEUTLER B., PETERHANS E.;
RT "Porcine tumor necrosis factor alpha: cloning with the polymerase
RT chain reaction and determination of the nucleotide sequence."
RL GENE 81:185-191(1989).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
CC EMBL; X54001; G2136; -.
CC DR EMBL; X54859; G2134; -.
CC DR EMBL; X57321; G2138; -.
CC DR EMBL; M29079; G164695; -.
CC DR PIR; S12606; S12606.
CC DR PIR; S17290; S17290.
CC DR PIR; S18965; S18965.
CC DR PROSITE; PS00251; TNF_1; 1.
CC DR PROSITE; PS50049; TNF_2; 1.
CC DR PFAM; PF00229; TNF; 1.
CC DR HSP; P01375; 2TUN.
KW CYTOKINE; CYTOTOXIN; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
FT PROPEP 1 76
FT CHAIN 77 232 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 144 176 BY SIMILARITY.
SQ SEQUENCE 232 AA; 25254 MW; 98540B7D CRC32;

Query Match 6.68; Score 104; DB 1; Length 232;
Best Local Similarity 39.08; Pred. No. 3.28e-02;
Matches 16; Conservative 10; Mismatches 13; Indels 2; Gaps 2;

Db 109 NALLANGVKLDNQLVVPDGLIILYISQVLFGRGCGPSTNV 149
QY 99 DGIL-HGVRYQDGNLVIOFPGLYFIICQLQFLVQ-CPNNSV 137

RESULT 15
ID TNFA_MACFA STANDARD; PRT; 233 AA.
AC P79337;

Search completed: Fri Aug 13 16:53:00 1999
Job time : 15 secs.

MPSRCH_PP protein - protein database search, using Smith-Waterman algorithm

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(TM)

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Aug 13 16:53:17 1999; MasPar time 15.54 Seconds
Tabular output not generated. 755.021 Million cell updates/sec
Title: >US-09-079-785-23
Description: (1-215) from US09079785.pep
Perfect Score: 1566
Sequence: 1 MHVPAGSVASHLGTSTRSYF.....DTSTFPLENLSIFLYSNSD 215

Scoring table: PAM 150
Gap 11
Searched: 179066 seqs, 54579741 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: sptrmb19
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus
Statistics: Mean 44.549; Variance 86.093; scale 0.517

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	1531	97.8	234	4	CD30L PROTEIN.	1.03e-296	
2	117	7.5	479	11	PHOSPHOPROTEIN PHOSPHA	2.13e-03	
3	117	7.5	499	11	PROTEIN PHOSPHATASE 5.	2.13e-03	
4	116	7.4	279	11	FAS LIGAND.	2.96e-03	
5	109	7.0	332	10	RIBITOL DEHYDROGENASE	2.91e-02	
6	109	7.0	1165	5	SIMILARITY TO PROTEIN-	2.91e-02	
7	108	6.9	157	4	TUMOR NECROSIS FACTOR	4.01e-02	
8	106	6.8	249	4	TWEAK.	7.56e-02	
9	102	6.5	240	4	LIGAND FOR HERPESVIRUS	2.63e-01	
10	102	6.5	240	4	TUMOR NECROSIS FACTOR	2.63e-01	
11	102	6.5	432	13	PROTEIN PHOSPHATASE 5	2.63e-01	
12	101	6.4	225	11	TNF-RELATED WEAK INDUC	3.57e-01	
13	98	6.3	104	6	TNFA (FRAGMENT)	8.85e-01	
14	99	6.3	233	6	TUMOR NECROSIS FACTOR	6.55e-01	
15	98	6.3	233	6	TUMOR NECROSIS FACTOR	8.85e-01	
16	98	6.3	619	3	CHROMOSOME XV READING	8.85e-01	
17	98	6.3	724	10	HYPOTHETICAL 82.5 KD P	8.85e-01	
18	99	6.3	1010	5	F5C5.4 PROTEIN.	6.55e-01	
19	99	6.3	1684	4	WUGSC-HDJ1186C01.1 PR	6.55e-01	
20	97	6.2	233	11	TUMOR NECROSIS FACTOR	1.19e-00	

TUMOR NECROSIS FACTOR-
TRANSPOSASE.
ATP SYNTHASE A CHAIN (P
HYPOTHETICAL 38.0 KD P
SPINDLY.
DNA POLYMERASE (EC 2.7
SULFONYLUREA RECEPTOR
SULFONYLUREA RECEPTOR
HYPOTHETICAL 30.3 KD P
F40F12.4 PROTEIN.
ANTI-MULLERIAN HORMONE
CODED FOR BY C. ELEGAN
TUMOR NECROSIS FACTOR.
F40H7.1 PROTEIN.
TUMOR NECROSIS FACTOR
HYPOTHETICAL 32.4 KD P
COSMID K12D9.
GYRASE BETA SUBUNIT (F
PC717R.
PEROXISOME BIOGENESIS
SULFONYLUREA RECEPTOR.
SULFONYLUREA RECEPTOR.
PHOSPHORIBOSYLAMINOIM
SULFONYLUREA RECEPTOR
C11D2.6 PROTEIN.

ALIGNMENTS

RESULT 1
ID 043404 PRELIMINARY; PRT; 234 AA.
AC 043404; (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CD30L PROTEIN.
GN CD30L.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98007874.
RA CROAGER E.J., ABRAHAM L.J.;
RT "Characterisation of the human CD30 ligand gene structure.";
RL BIOCHIM. BIOPHYS. ACTA 1353:231-235(1997).
DR EMBL; AF006384; G2815515;
DR EMBL; AF006381; G2815515; JOINED.
DR EMBL; AF006382; G2815515; JOINED.
DR EMBL; AF006383; G2815515; JOINED.
DR PROSITE; PS00251; TNF-1; 1.
SQ SEQUENCE 234 AA; 25963 MW; B6137845 CRC32;
Query Match 97.8%; Score 1531; DB 4; Length 234;
Best Local Similarity 98.1%; Pred No. 1.03e-296;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 20 MHVPAGSVASHLGTSTRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLK 79
QY 1 MHVPAGSVASHLGTSTRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLK 60
Db 80 GNCSDDLCLIKRAPFKKSWAYLQVAKHLNKTLSWKNKDGILHGVYQDGNLVIOFPGLY 139
QY 61 GNCSDDLCLIKRAPFKKSWAYLQVAKHLNKTLSWKNKDGILHGVYQDGNLVIOFPGLY 120
Db 140 FIICQLQFLVCCPNNSVDLKKYELLINKHKKQXLVTVCSGMQTKHVYQNLISQFLLDYIQ 199
QY 121 FIICQLQFLVCCPNNSVDLKKYELLINKHKKQXLVTVCSGMQTKHVYQNLISQFLLDYIQ 180
Db 200 VNTTISVNDVTQYIDTSTFPLENVLSTFLXNSD 234
QY 181 VNTTISVNDVTQYIDTSTFPLENVLSTFLXNSD 215

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RESULT 2
ID O64538 PRELIMINARY; PRT; 479 AA.
AC O64538:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PHOSPHOPROTEIN PHOSPHATASE (FRAGMENT).
OS RATTUS NORVEGICUS (RAT)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=LUNG;
RX MEDLINE: 95062208.
RA CHINKERS M.;
RT targeting of a distinctive protein-serine phosphatase to the protein
RL kinase-like domain of the atrial natriuretic peptide receptor.
;
RL PROC. NATL. ACAD. SCI. U.S.A. 91:11075-11079(1994).
DR EMBL: U12203; G1663530;
DR PFAM: PF00149; Stposphatase; 1.
DR PFAM: PF00515; TPR; 2.
FT NON_TER 1
SQ SEQUENCE 479 AA; 54718 MW; 0F812560 CRC32;

Query Match 7.5%; Score 117; DB 11; Length 479;
Best Local Similarity 28.1%; Pred. No. 2.13e-03;
Matches 25; Conservative 27; Mismatches 29; Indels 8; Gaps 8;

Db 188 CAYQILVQV-KE-V-LCKLSTLVTETLKEKITVC-GDTHG-QFYDLLNIFELNGLPSE 242
QY 124 CQLQFLVQCPNNSVDL-KLELLINKHKQALVTVCESGMQTKHVYQNSLQFLLDYLVQV 182

Db 243 TNPYI-FNG-DFVDRGSFSFVILTFGF 269
QY 183 TTISVNVDTFQYIDTSTFFLENVLSIFLY 211

RESULT 3
ID O35299 PRELIMINARY; PRT; 499 AA.
AC O35299:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PROTEIN PHOSPHATASE 5.
GN PP5.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA OLLENDORFF V., DONOGHUE D.J.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF018262; G2407637;
DR PFAM: PF00149; Stposphatase; 1.
DR PFAM: PF00515; TPR; 2.
SQ SEQUENCE 499 AA; 56846 MW; 46E531D4 CRC32;

Query Match 7.5%; Score 117; DB 11; Length 499;
Best Local Similarity 28.1%; Pred. No. 2.13e-03;
Matches 25; Conservative 27; Mismatches 29; Indels 8; Gaps 8;

Db 208 CAYQILVQV-KE-V-LCKLSTLVTETLKEKITVC-GDTHG-QFYDLLNIFELNGLPSE 262
QY 124 CQLQFLVQCPNNSVDL-KLELLINKHKQALVTVCESGMQTKHVYQNSLQFLLDYLVQV 182

Db 263 TNPYI-FNG-DFVDRGSFSFVILTFGF 289
QY 183 TTISVNVDTFQYIDTSTFFLENVLSIFLY 211

RESULT 4
ID O61217 PRELIMINARY; PRT; 279 AA.
AC O61217:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FAS LIGAND.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA FENNER M.H., SHIODA T., ISSELBACHER K.J.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U58995; G1389772;
DR PROSITE: PS00251; TNF_1; 1.
DR PFAM: PF00229; TNF; 1.
SQ SEQUENCE 279 AA; 31340 MW; 9062DF08 CRC32;

Query Match 7.4%; Score 116; DB 11; Length 279;
Best Local Similarity 35.4%; Pred. No. 2.96e-03;
Matches 23; Conservative 9; Mismatches 29; Indels 4; Gaps 4;

Db 145 AHLTGNPHSRISPLEWEDTYGTALISGVYKKGVLVINEAGLYFYVSKVYFVGSCNNQP 204
QY 81 AYLVQVAKHLNKTLSWKNK-GI-L-HGVRYODGNLVIOFGLYFIICQLQLVQ-CPNNS 136

Db 205 LNHKV 209
QY 137 VDLKL 141

RESULT 5
ID O22985 PRELIMINARY; PRT; 332 AA.
AC O22985:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE RIBITOL DEHYDROGENASE ISOLOG.
GN T19F06.14.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; VIRIDIPANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
RA SPRIGGS T.A., MASON T.M., KERLAVAGE A.R., ADAMS M.D., SOMERVILLE C.R.,
RA VENTER J.C.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AC002343; G2262111;
DR PFAM: PF00106; adh_short; 1.
SQ SEQUENCE 332 AA; 35840 MW; A4E08F03 CRC32;

Query Match 7.0%; Score 109; DB 10; Length 332;
Best Local Similarity 33.3%; Pred. No. 2.91e-02;
Matches 19; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

Db 108 ESDLPLNLLNINAGLAHEHAISEDGIENTFATNYLGHFLNLLNLLKMIQTAEET 164
QY 135 NSVDLKELELLINKHKQALVTVCESGMQTKHVYQNSLQFLLDYLVQNTTISVNDT 191

RESULT 6
ID O01923 PRELIMINARY; PRT; 1165 AA.
AC O01923:
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SIMILARITY TO PROTEIN-TYROSINE PHOSPHATASES.
GN R155.3.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
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Db 65 KGQCPSTHVL 76
| | | |
QY 129 LVQ-CPNNSVDL 139

RESULT 8
ID O43508 PRELIMINARY; PRT; 249 AA.
AC O43508;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TWEAK.
DN APO3L.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-TONSIL;
RX MEDLINE; 98070415.
RA CHICHEPORTICHE Y., BOURDON P.R., XU H., HSU Y.-M., SCOTT H.,
RA HESSON C., GARCIA I., BROWNING J.L.;
RT "TWEAK, a new secreted ligand in the tumor necrosis factor family
that weakly induces apoptosis.";
RL J. BIOL. CHEM. 272:32401-32410(1997).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE; 98228355.
RX MARSTERS S.A., SHERIDAN J.P., PITTI R.M., BRUSH J., GODDARD A.,
RA ASHKENAZI A.;
RT "Identification of a ligand for the death-domain-containing receptor
Apo3.";
RL CURR. BIOL. 8:525-528(1998).
DR EMBL; AF030099; G2707219; -;
DR EMBL; AF055872; G3108231; -;
SQ SEQUENCE 249 AA; 27216 MW; 3AEC1F1 CRC32;

Query Match 6.8%; Score 106; DB 4; Length 249;
Best Local Similarity 35.9%; Pred. No. 7.56e-02;
Matches 14; Conservative 15; Mismatches 7; Indels 3; Gaps 2

Db 149 QIGEIFVTRAGLYLYXCOVHF--D-EGKAVYKLDLVD 184
| | | | : | | | | | | | | : | | | | | | | |
QY 108 QDGNLVIFQFGLYFIIQCLOFLVQCPNNSVDLKLELLIN 146

RESULT 9
ID O75476 PRELIMINARY; PRT; 240 AA.
AC O75476;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE LIGAND FOR HERPESVIRUS ENTRY MEDIATOR.
DN HVEM-L.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
[1]
RN SEQUENCE FROM N.A.
RP HARROP J.A., McDONNELL P.C., BRIGHAM-BURKE M., LYN S.D., MINTON J.,
RA TAN K.B., DEDE K., SPAMPANATO J., SILVERMAN C., HENSLEY P.,
RA DIPRINZIO R., EMERY J.G., DEEN K., EICHMAN C., CHABOT-FLETCHER M.,
RA TRUNEH A., YOUNG P.R.;
RT "HVEM-L, a novel ligand for HVEM/TR2, stimulates NF-kB-dependent
transcription, proliferation of T cells and inhibition of HI29 cell
growth.";
RL SUBMITTED (JUL-1998), TO EMBL/GENBANK/DBJ DATA BANKS.
[2]
RN SEQUENCE FROM N.A.
RP SHINTANI Y., NISHI K., LYN S.D., YOUNG P.R.;
RA SUBMITTED (MAY-1998), TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF064090; G3283356; -;
SQ SEQUENCE 240 AA; 26350 MW; 3490EB77 CRC32;

RESULT 12

MACROPUS EUGENII (TAMMAR WALLABY) .
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; METATHERIA;

OC DIPROTODONTIA; MACROPODIDAE; MACROPUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY-ASSOCIATED LYMPH NODE;
RA HARRISON G.A., BROUGHTON M.J., DEANE E.M., COOPER D.W.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF059515; G3659513; -.
DR PROSITE; PS00251; TNF_1; 1.
SQ SEQUENCE 233 AA; 25696 MW; 584C4ELE CRC32;

Query Match 6.3%; Score 99; DB 6; Length 233;
Best Local Similarity 31.7%; Pred. No. 6.55e-01;
Matches 19; Conservative 14; Mismatches 22; Indels 5; Gaps 4;

Db 93 IADPLAEGKQLWLRANRANLSDVMDLVNOLVVPSTGLVLYSQLLFKGEDCANEPILL 152
QY 85 VAKHLNKTLSW-NK-DGIL--HGVRYQDGNLVIOFFGLYFIICQLQLVQ-CPNNSVDL 139

RESULT 15
ID Q18779 PRELIMINARY; PRT; 233 AA.
AC Q18779;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR ALPHA.
GN TNFA.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; BOS.
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N'DAMA;
RA IRAQI F.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF011926; G2599343; -.
DR PROSITE; PS00251; TNF_1; 1.
DR PFAM; PF00229; TNF; 1.
SQ SEQUENCE 233 AA; 25395 MW; 64FAFC88 CRC32;

Query Match 6.3%; Score 98; DB 6; Length 233;
Best Local Similarity 38.9%; Pred. No. 8.85e-01;
Matches 14; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

Db 115 NGVKLEDNQLVVPADGLYLIYSQVLFRCGQCPSTPL 150
QY 103 HGVRYQDGNLVIOFFGLYFIICQLQLVQ-CPNNSV 137

Search completed: Fri Aug 13 16:54:02 1999
Job time : 45 secs.